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Supplementary Materials for

HIV-1 therapy with monoclonal antibody 3BNC117 elicits host immune responses against HIV-1

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Materials and Methods

Study participants

Study participants that received 3BNC117 were all part of the 3BNC117 Phase-I open-label clinical trial NCT02018510 (*16*). The protocol was approved by the Federal Drug Administration in the USA, the Paul Ehrlich Institute in Germany and the Institutional Review Boards at the Rockefeller University, the University of Cologne, Weill Cornell Medical College and the Brigham and Women's Hospital Boston. The control cohort of untreated viremic HIV-1-infected subjects were study participants in Seattle Vaccine Unit Observational Protocols 4712 and 4325 (P.I. MJ McElrath). Subjects were recruited from the Seattle, WA community through advertisements and referrals from care providers. All participants provided written informed consent before participation in the studies and the studies were conducted in accordance with Good Clinical Practice.

ELISA of 3BNC117 serum levels

3BNC117 serum concentrations were determined using a validated sandwich ELISA as previously described (*16*). Lower limit of accuracy of the ELISA assay was determined to be 2 μg/ml. Patients for whom background > 0.50 μg/ml at Day 0 baseline was detected (Subjects 2A4, 2B3, 2C2, 2C4, 2C1 and 2E2) were excluded from the illustration of 3BNC117 serum levels shown in Figure 1A.

Virus cultures

Virus from study participants was obtained by co-culture of patient peripheral blood mononuclear cells (PBMCs) with healthy donor PBMCs as previously described (*42*). Healthy donor PBMCs were obtained from patients by leukapheresis under study protocol MNU-0628 at Rockefeller University. All donors provided written informed consent before participation. Healthy donor PBMCs were pre-stimulated at a density of 5 x 10^6 cells ml^{-1} in IMDM containing 10% FBS, 1% Penicillin-Streptomycin and PHA at 1 μg ml^{-1} for 2-3 days at 37°C and 5% CO_2. 6 x 10^6 of the stimulated donor PBMCs were then transferred to IMDM containing 10% FBS, 1% Penicillin-Streptomycin, 10 IU IL-2 ml^{-1} and 5 μg ml^{-1} polybrene and co-cultured with 5-10 x 10^6 patient PBMCs at 37°C and 5% CO_2. Media was replaced weekly and the presence of p24 in culture supernatant was quantified by Lenti-X p24 Rapid Titer Kit (Clontech). Cultures exceeding 1 ng/ml of p24 per ml of supernatant were frozen and stored at -80°C. Determination of tissue culture infectious dose 50 ($TCID_{50}$) and subsequent testing for sensitivity of autologous viruses to different broadly neutralizing antibodies and autologous serum IgG was carried out using a TZM.bl neutralization assay according to established protocols (*43, 44*). All neutralization assays were run in duplicates.

Antibody neutralization testing by TZM.bl

To determine heterologous neutralizing activity, patient sera or purified IgG were tested against a defined panel of pseudoviruses in TZM.bl assay as previously described (*21, 43*). IgG was purified from patient plasma using Protein G Sepharose 4 Fast Flow according to manufacturer's instructions. All neutralization assays were conducted in a laboratory meeting Good Clinical Laboratory Practice (GCLP) Quality Assurance criteria

(Michael S. Seaman, Beth Israel Deaconess Medical Center). Samples from 3BNC117-treated patients and controls were tested in intermingled batches at a variety of different time points. All neutralization assays were run in duplicates.

Antibody-strain coverage curves

Total IgG coverage curves ((1/AUC) vs. percent of strains neutralized) were generated using Antibody database v2.0 (*45*).

Area under the curve calculation of antibody neutralization

The area under the curve (AUC) was calculated using the neutralization (y-axis) at a particular measured concentration level (x-axis) using the R package flux (version 0.2.1.). In order to have equal distance between concentration levels, concentration levels were logarithmized using the natural logarithm. Since mean neutralization activity of both treated and the control group towards murine leukemia virus (MuLV) was around 7%, a neutralization of 10% was considered background noise. In addition, we tested at which concentration level the standard deviation (sd) of the assay exceeded variation due to neutralization. For neutralization by total IgG, only concentrations greater than 6.173 ug/ml were taken into consideration since the measurement variation exceeded changes in antibody neutralization below this level (i.e. concentration levels used to calculate AUCs were 500 µg/ml, 166.667 µg/ml, 55.556 µg/ml, 18.519 µg/ml and 6.173 µg/ml).

Statistical tests of heterologous neutralization AUC data

In Figure 2A, mean AUC difference values of off/on-ART patients were compared to mean AUC differences of control patients with an unpaired Wilcoxon test (rank-sum test).

For Figure 2B pairwise testing was performed if AUC difference values are different for different groups (i.e., control group, treated while off-ART, and treated while on-ART). The model was built using generalized estimating equations for a model with intercept and group as the only covariate (*38*). Equicorrelated measurements within a cluster (patient) were assumed and normal distribution was used. p-values were estimated for the null-hypothesis that the weight parameter of the group covariate is zero. GEEQBOX version 1.0 was used for calculations (*38*).

For Figure 2D, AUC difference values of controls were compared to the AUC difference values of the off-ART (panel 2) or on-ART (panel 3) 3BNC117-treated patients using an unpaired Wilcoxon test (rank-sum test). This was performed for each virus separately. A star is shown if the p-value was significant after Bonferroni correction ((p-value <= (0.05 / # tests)) = (p-value <= 0.003846154)).

To exclude that leftover amounts of 3BNC117 could explain the neutralization increase observed in 3BNC117-treated individuals, the Spearman rank correlation of neutralization changes in each patient with the neutralization profile of 3BNC117 was calculated (Fig. S5, Table S8). Rank correlation was calculated using both IC_{50} and AUC values. p-values were corrected for multiple testing by Bonferroni-correction (p-value <= (0.05 / # tests)) = (p-value <= 0.0019)).

Analysis of confounding variables

To determine whether the observed difference in AUC improvement between 3BNC117-treated individuals and viremic controls was confounded by variables such as age, time of infection and starting AUC, a systematic confounder analysis was performed. For each variable and each virus (Table S7), we tested whether the variable is predictive for the observed AUC difference. To do so, a linear regression model (intercept only/null model) was compared to an extended model that considered the variable in question. A likelihood ratio test asking whether the extended model is superior to the linear model was performed (Table S7). To compute the bayes factors for the likelihood ratio test, the R package BayesFactor (version 0.9.2) was used. A total of 8 features was tested across each of 13 viruses (total = 104 tests).

Single genome sequencing (SGS) of HIV-1 *env* genes

HIV-1-RNA was extracted from patient plasma using the Qiagen MinElute Virus Spin Kit according to manufacturer's instructions. Extracted RNA was subjected to env-specific cDNA Synthesis using SuperScript III Reverse Transcriptase and primer envB3out 5'– TTGCTACTTGTGATTGCTCCATGT 3'. Remaining RNA was digested using RNAseH for 20 minutes at 37 °C before diluted cDNA was subjected to two-rounds of nested PCR with gp160-specific primers. First round PCR was performed in a 20 ul volume containing 1x High Fidelity buffer, 2 mM MgSO4, 0.2 mM dNTPs and 0.5 units of High Fidelity Platinum Taq using 0.2 uM each of primers envB5out 5'TAGAGCCCTGGAAGCATCCAGGAAG 3' and envB3out 5' TTGCTACTTGTGATTGCTCCATGT 3'. PCR conditions were 94 °C, 2min; (94 °C, 15s; 55 °C 30s; 68 °C, 4min) x 35; 68 °C, 15min. Second round PCR was performed using 1 ul of PCR 1 and 0.2 uM of primers of envB5in 5' TTAGGCATCTCCTATGGCAGGAAGAAG 3' and envB3in 5'– GTCTCGAGATACTGCTCCCACCC 3'. PCR conditions were the same as PCR-1 except for 45 cycles and an increased annealing temperature of 58 °C. PCR2 products were checked using 1% 96-well E-Gels (Invitrogen). Bands from PCRs with amplification efficiencies lower than 30% were subjected to library preparation using the Illumina Nextera DNA Sample Prepration Kit (Illumina) as described (*46*). Briefly, 10 ng of DNA per band were subjected to tagmentation, ligated to barcoded sequencing adapters using the Illumina Nextera Index Kit and then purified using AmPure Beads XP (Agencourt). 96 different purified samples were pooled into one library and then subjected to paired-end MiSeq Sequencing using the Illumina Miseq Nano 300 cycle kits at a concentration of 12 pM.

Bioinformatic processing of MiSeq env-sequences

Sequence adapters were removed using Cutadapt v1.8.3. Read assembly for each virus was performed in three steps. First, de novo assembly was performed using Spades v3.6.1 to yield long contig files. Contigs longer than 255bp were subsequently aligned to an HIV envelope reference sequence and a consensus sequence was generated using Geneious 8. Finally, reads were re-aligned to the consensus sequence to close gaps and a final consensus was generated. Sequences with double peaks (cutoff consensus identity for any residue <75%) were omitted from downstream analyses.

Analysis of viral evolution

Alignments of *env* nucleotide sequences were generated using ClustalW (version 2.11) (*47*) or via manual alignment using Geneious (version 8.1.6) sequence analysis software (*48*). Regions that could not be unambiguously aligned were removed for phylogenetic analysis and diversity calculations. Evolutionary model classes for maximum likelihood phylogenetic analyses were selected using jModelTest (*49*). Maximum likelihood phylogenetic trees were generated using PhyML (version 3) (*50*) with joint estimation of model parameter values and phylogenies. Within-patient trees were midpoint rooted and colored using the Rainbow Tree webtool through the Los Alamos National Laboratory (LANL) HIV Database (http://www.hiv.lanl.gov/content/sequence/RAINBOWTREE/rainbowtree.html). Pairwise genetic distances were calculated using PhyML (*50*) in the DIVEIN webtool (http://indra.mullins.microbiol.washington.edu/DIVEIN/diver.html) (*41*) using the Jukes-Cantor model of nucleotide substitution or the HIVw model of amino acid substitution (*51*). Pairwise genetic diversity was compared among samples using a two-sample U-statistic test (*39, 40*) in the DIVEIN webtool (*41*).

Highlighter plots were generated using the LANL nucleotide and amino acid Highlighter tools (http://www.hiv.lanl.gov/content/sequence/HIGHLIGHT/highlighter_top.html). To generate Day 0 consensus sequences, each site was assigned the residue present in the highest frequency in Day 0 sequences. Gaps were treated as characters and sites without a single, most common residue were assigned "X."

Longitudinal modified weblogo plots of 3BNC117 contacts were generated using LASSIE (Longitudinal Antigenic Sequences and Sites from Intrahost Evolution) (*28*). Sites under significant selection (cutoff ≥80% new amino acid residue in particular position relative to Day 0 consensus) were determined and graphed using LASSIE.

Generation of CMV-env based pseudoviruses

CMV-env expression cassettes were generated according to an established protocol (*52*). Briefly, the CMV promoter was amplified from pcDNA 3.1D/V5-His-TOPO Expression vector using the primers CMVenv 5'AGTAATCAATTACGGGGTCATTAGTTCAT 3'and CMVenv1A 5'CATAGGAGATGCCTAAGCCGGTGGAGCTCTGCTTATATAGACCTC 3'. The PCR product was purified using the Macherey-Nagel PCR and Gel Purification Kit.

1 ul of first round PCR product was amplified using primers env1ATOPO 5' CACC GGCTTAGGCATCTCCTATGGCAGGAAGAA 3' and Rev19 5' ACTTTTTGACCACTTGCCACCCAT 3' in a 20 ul volume containing 1x High Fidelity Buffer, 2 mM MgSO4, 0.2 mM dNTPs, 0.5 units of High Fidelity Platinum and 0.2 uM of each primer. Cycling conditions were 94 °C, 2min; (94 °C, 15s; 55 °C 30s; 68 °C, 4min) x 35; 68 °C, 10min. The presence of env was validated by analysis on a 0.7% Agarose gel and the product was purified using the Macherey-Nagel Gel and PCR Purification Kit. 10 ng of envelope and 0.5 ng of CMV were then subjected to overlapping PCR with primers CMVenv and Rev19 in triplicates. Total reaction volume

was 50 ul containing 1x High Fidelity Buffer, 0.2 uM MgS04, 0.2 mM dNTPs, 1 U of Platinum Taq High Fidelity and 0.4 uM of each primer. PCR was carried out at 94 °C, 2min; (94 °C, 30s; 60 °C 30s; 68 °C, 4min) x 25; 68 °C, 10min. 500 ng of CMV-env were co-transfected with pSG3Δenv in 6-well plates into 293T cells and supernatant was harvested after 48h. Supernatants were subjected to neutralization testing by TZM.bl as described above.

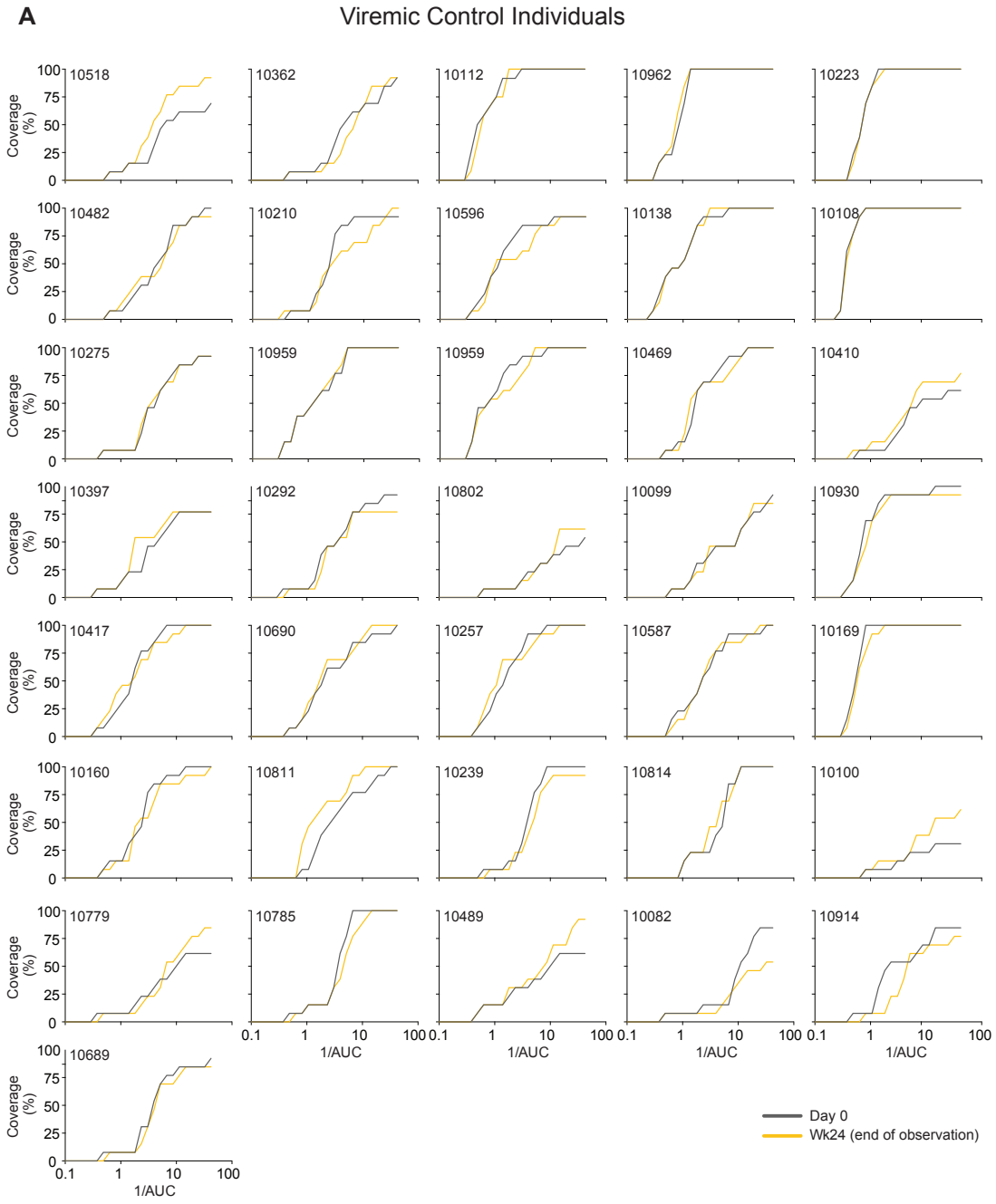

Fig. S1.

Dynamics of neutralization potency and breadth in each individual. Graphs show relationship between neutralization potency (1/AUC, x-axis) and breadth of neutralization (% of strains neutralized, y-axis) on Day 0 (grey) and at end of observation period (respective color for each group of study). **A**. untreated viremic control individuals (yellow). **B**. 3BNC117-treated individuals off-ART (dark blue) and 3BNC117-treated individuals on-ART (light blue)

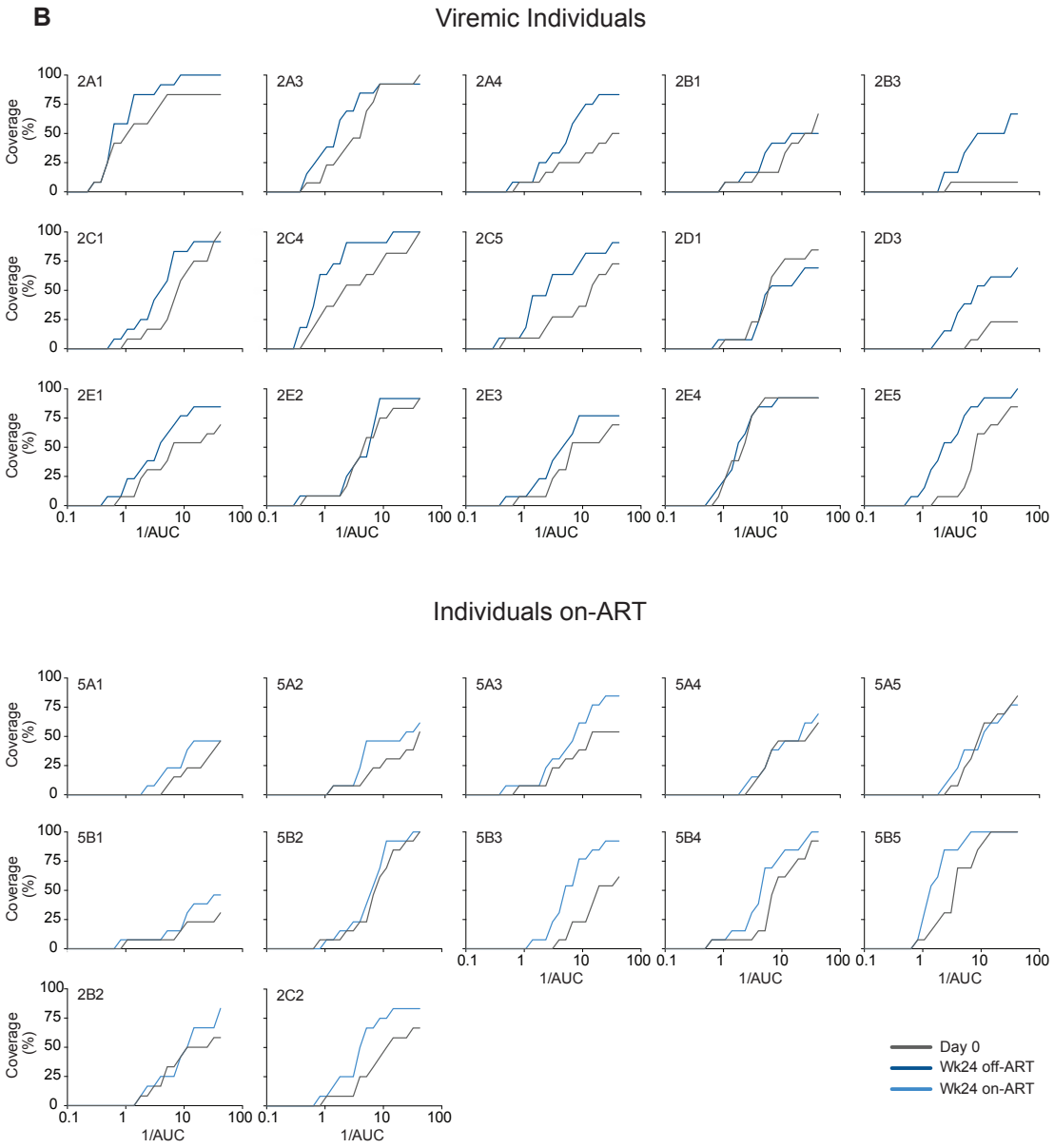

Fig. S1., continued

Dynamics of neutralization potency and breadth in each individual. Graphs show relationship between neutralization potency (1/AUC, x-axis) and breadth of neutralization (% of strains neutralized, y-axis) on Day 0 (grey) and at end of observation period (respective color for each group of study). **A**. untreated viremic control individuals (yellow). **B**. 3BNC117-treated individuals off-ART (dark blue) and 3BNC117-treated individuals on-ART (light blue)

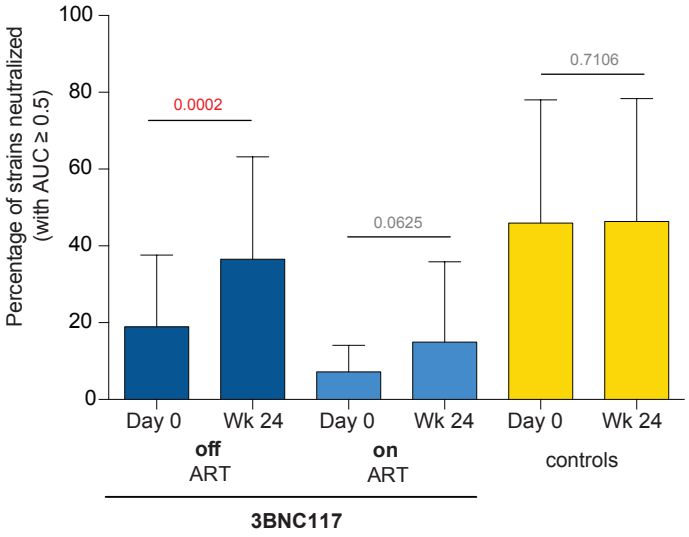

Fig. S2.

Dynamics of neutralization breadth by group of study. Bar plot illustrating the mean percentage of viruses neutralized (cutoff AUC ≥ 0.5) on Day0 and at the end of observation period by group of study. p-values determined using two-tailed Wilcoxon signed-rank test (red = significant, grey = n.s.). Raw values in Table S5.

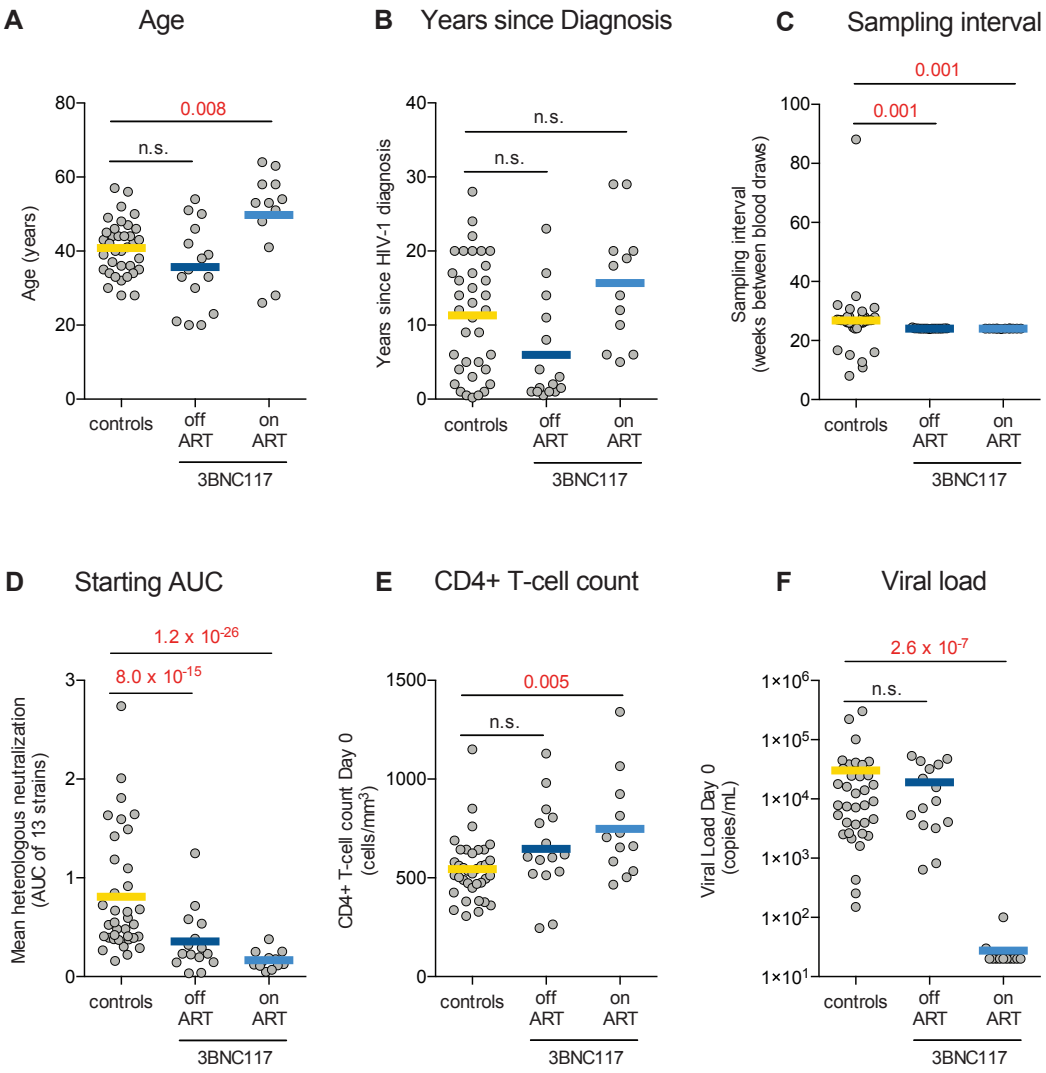

Fig. S3.

Comparison of clinical parameters between groups. Scatter dot plot of clinical parameters by patient group. Colored bars represent mean values of each group. p-values (indicated in red when significant) determined by unpaired Wilcoxon rank-sum test. Two hypotheses were tested for each parameter yielding a Bonferroni-corrected significance threshold of 0.025 with significance level $\alpha = 0.05$. n.s. = not significant. All parameters were tested in a confounder analysis and none of the parameter differences were found to be significant confounders (Table S7).

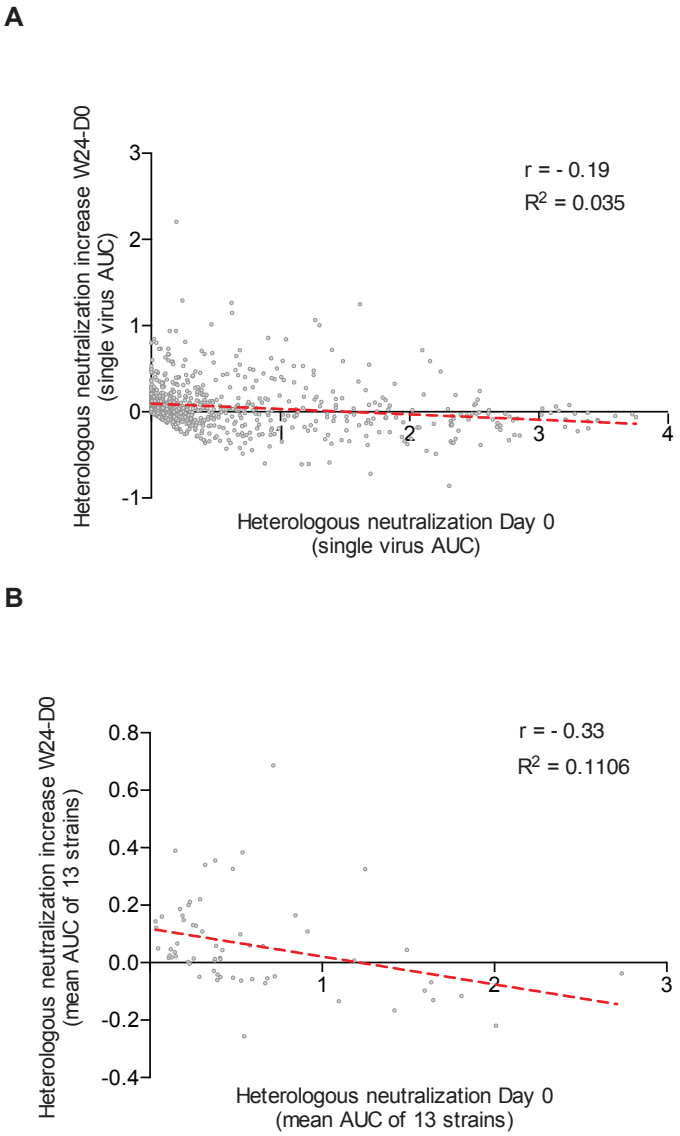

Fig. S4.

Correlation between starting AUC and AUC increase. **A.** Scatter plot of Day 0 AUC data (x-axis) and AUC difference W24-D0 (y-axis). Each dot shows the AUC data for a single virus from a single patient. **B.** Scatter plot of mean day 0 AUC data (x-axis) and mean AUC difference W24-D0 (y-axis). Each dot shows the mean data across all 13 viral strains for a particular patient. A linear fit model (dashed red line) is added with corresponding r and R2 in black at the top right.

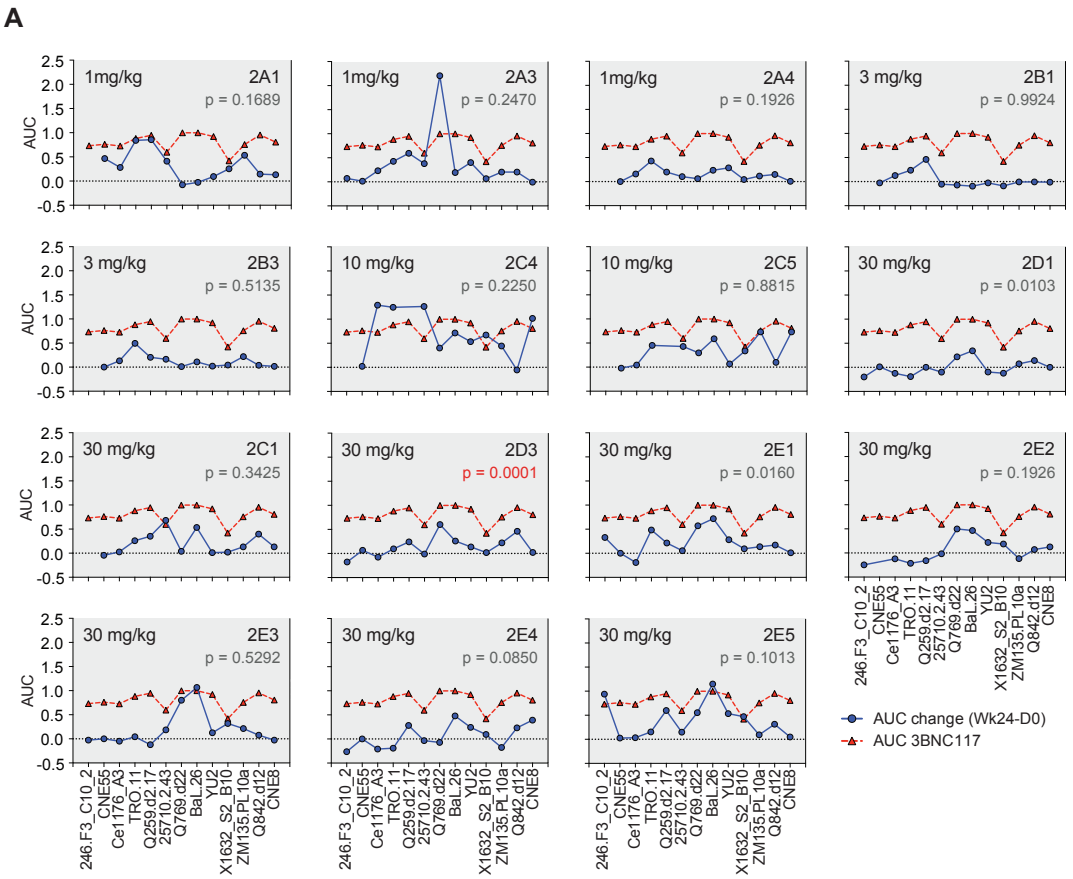

Fig. S5.

Neutralization profile comparison of AUC change in 3BNC117-treated individuals with neutralization profile of 3BNC117. For each individual the individual's AUC change (Wk24 - Day 0 AUC) against every strain is plotted in blue (**A.** viremic individuals, **B.** individuals on-ART). The AUC profile of 3BNC117 against those same strains is plotted in red as a comparator. The neutralization profiles were compared by assessing their Spearman rank correlation. p-values indicated in top right corner of graph (grey = n.s., red = significant). Bonferroni-corrected threshold: 0.0019. Full rank correlation and p-values in Table S8.

B

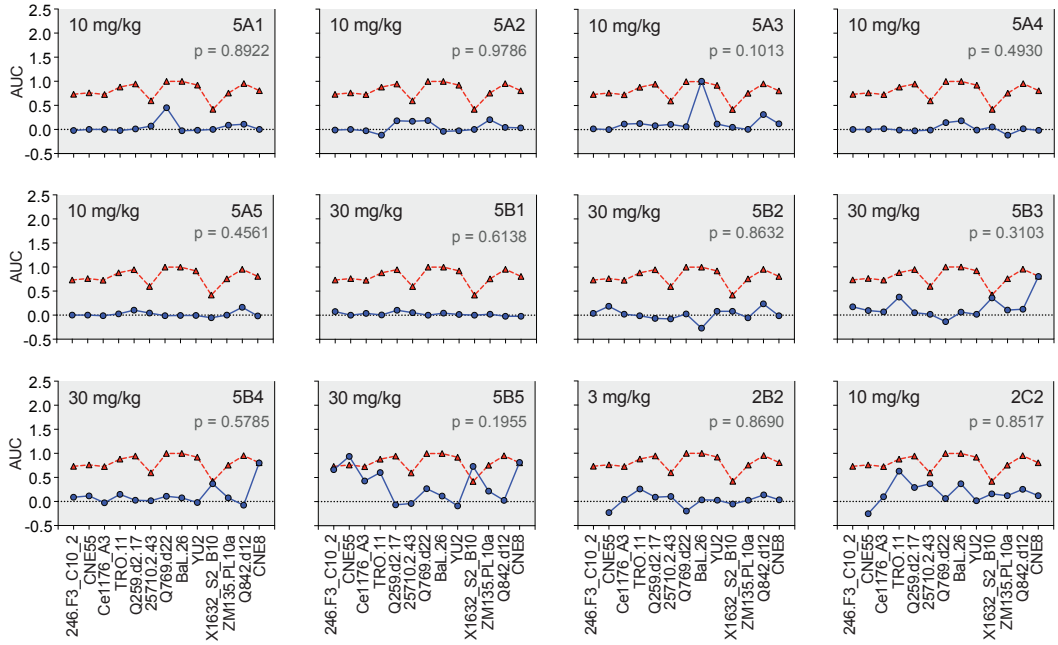

Fig. S5., continued

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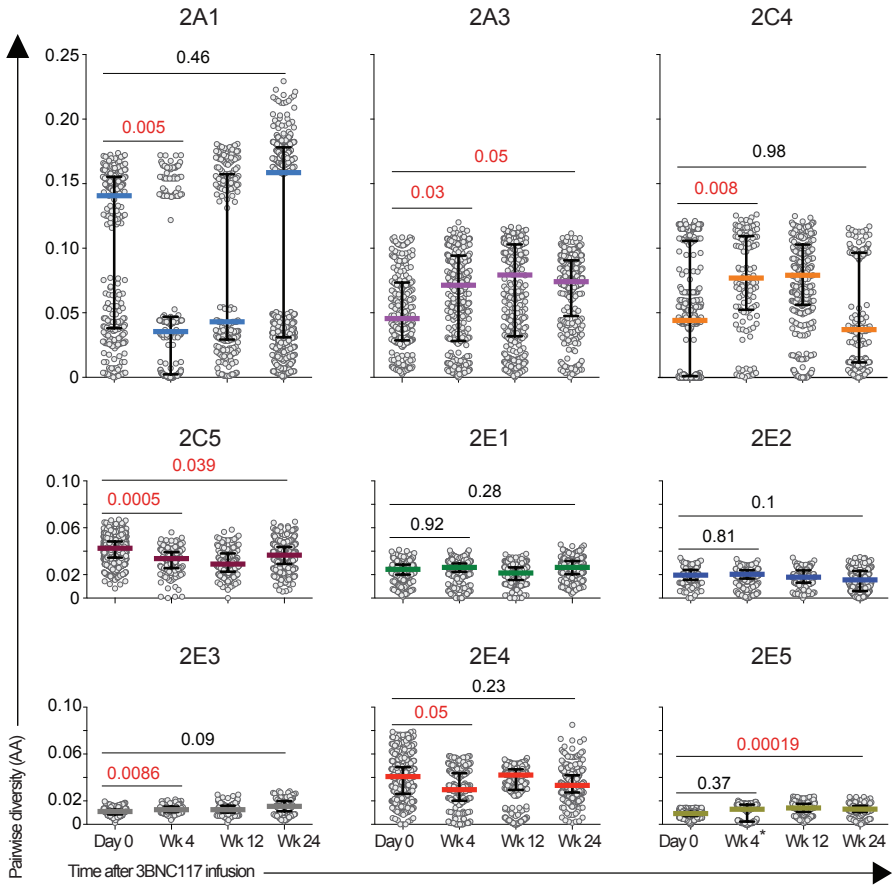

Fig. S6.

Pairwise diversity over time (amino acid level). Scatter plots depicting pairwise amino acid sequence diversity of plasma env sequences on d0, and wk 4 (*wk6 for 2E5), 12 and 24 after infusion. Each dot represents the pairwise genetic difference between two sequences at a given timepoint. Colored bars indicate median diversity, while black bars indicates the interquartile range. p-values were determined using a two-sample U-statistic based Z-test (*39-41*).

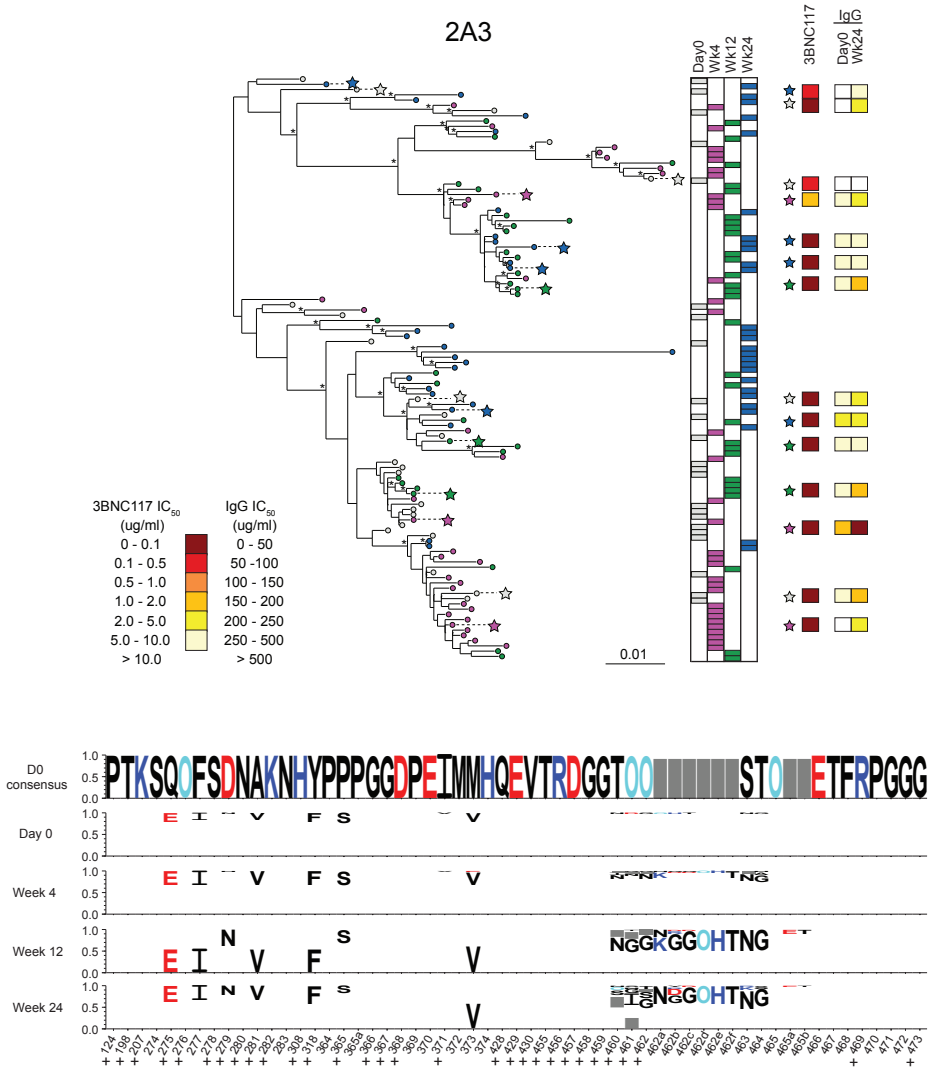

Fig. S7.

Viral evolution in subjects 2A3, 2C5, 2C4 and 2E2-2E5. **Top.** Maximum-likelihood phylogenetic trees of plasma-derived env sequences from respective subjects sampled on d0, wk4 (wk6 in case of 2E5), wk12 and wk24 after 3BNC117 infusion. Black asterisks indicate nodes with significant boostrap values (bootstrap support ≥ 70%). Bar graphs (middle) indicate the timepoints from which sequences were derived. Heat maps (right) show the 3BNC117 IC_{50}, d0 IgG IC_{50} and wk 24 IgG IC_{50} values against autologous envs as indicated by colored stars. **Bottom.** Weblogo plots that illustrate amino acid changes in and directly adjacent to 3BNC117 contact residues over time. White boxes indicate that sequence matches to the d0 consensus, grey boxes indicate gaps in alignment. Colors indicate basic (dark blue) and acidic (red) residues and a turquoise "O" is used instead of "N" to indicate a potential N-glycosylation site. Logo plots were generated using LASSIE (*28*). + symbols indicate contact residues confirmed by two crystal structures (*26, 27*).

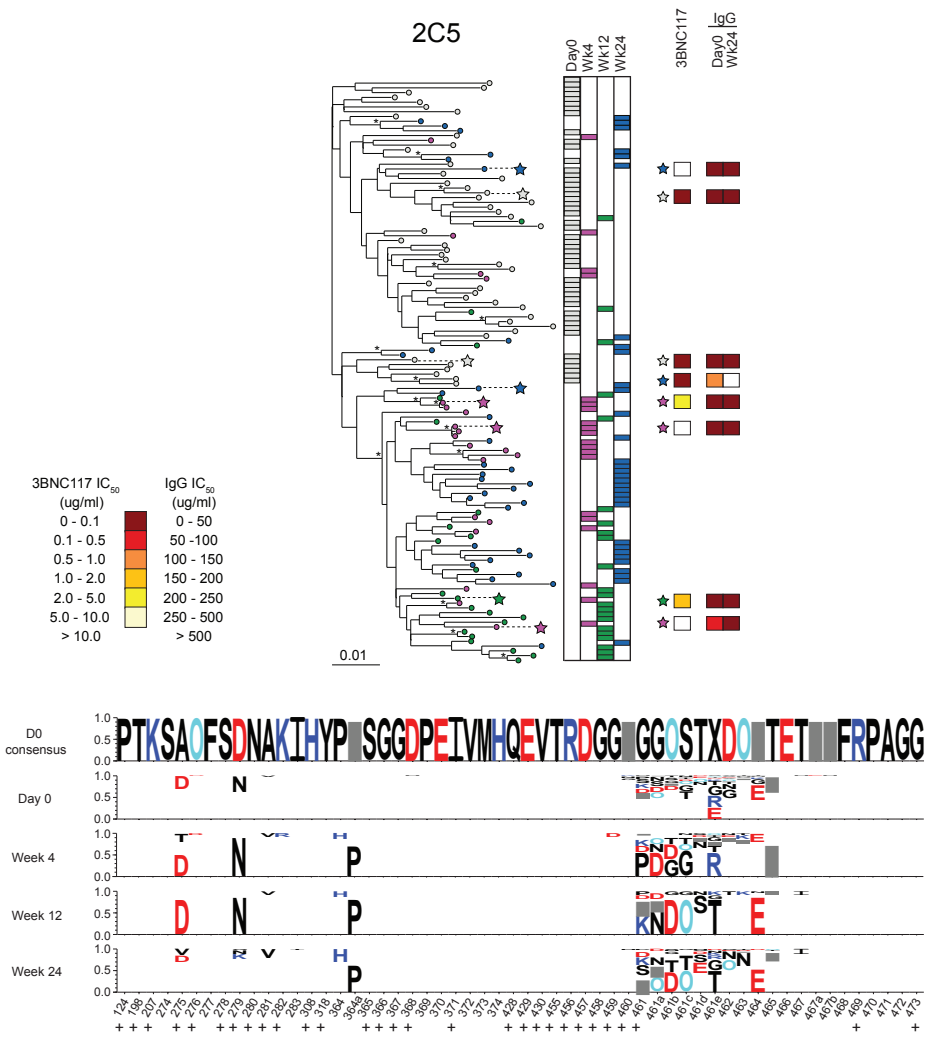

Fig. S7., continued

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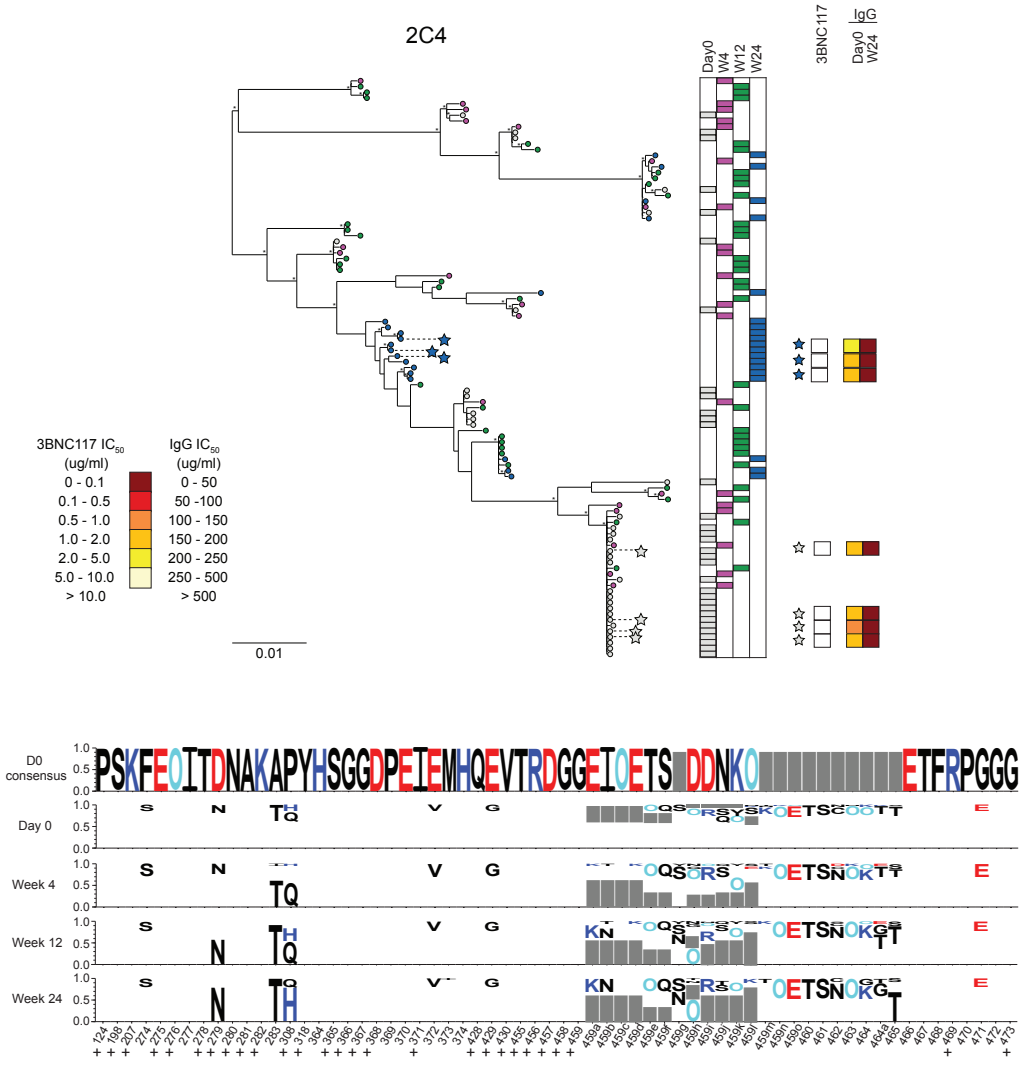

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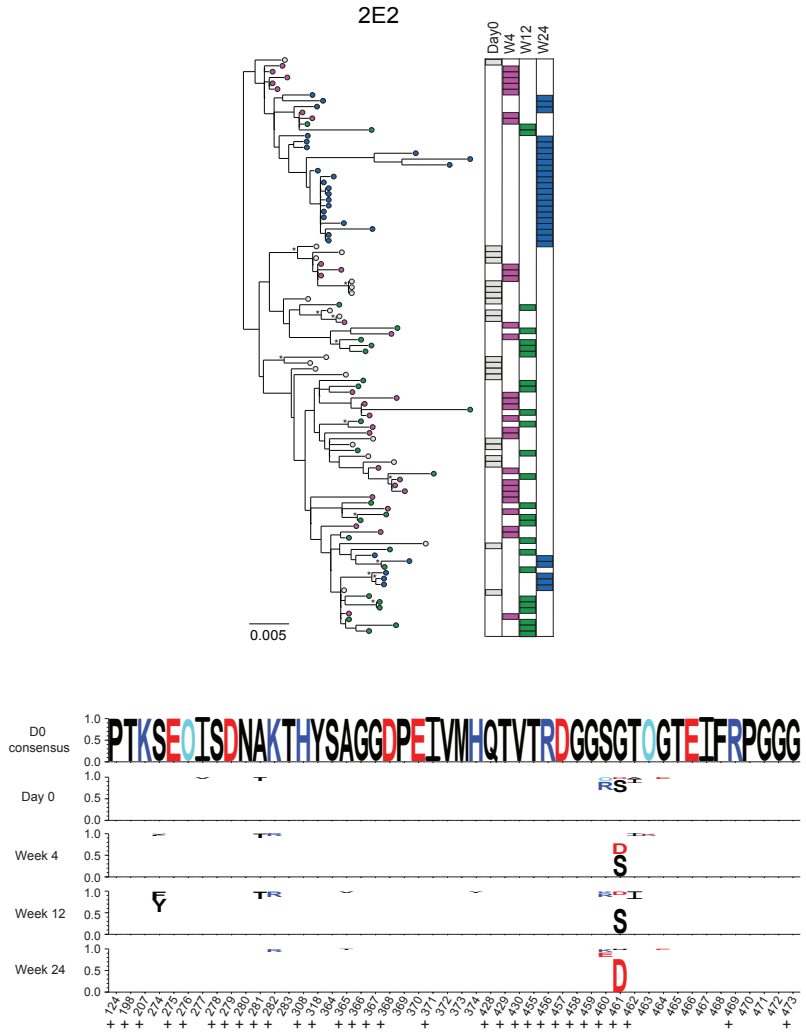

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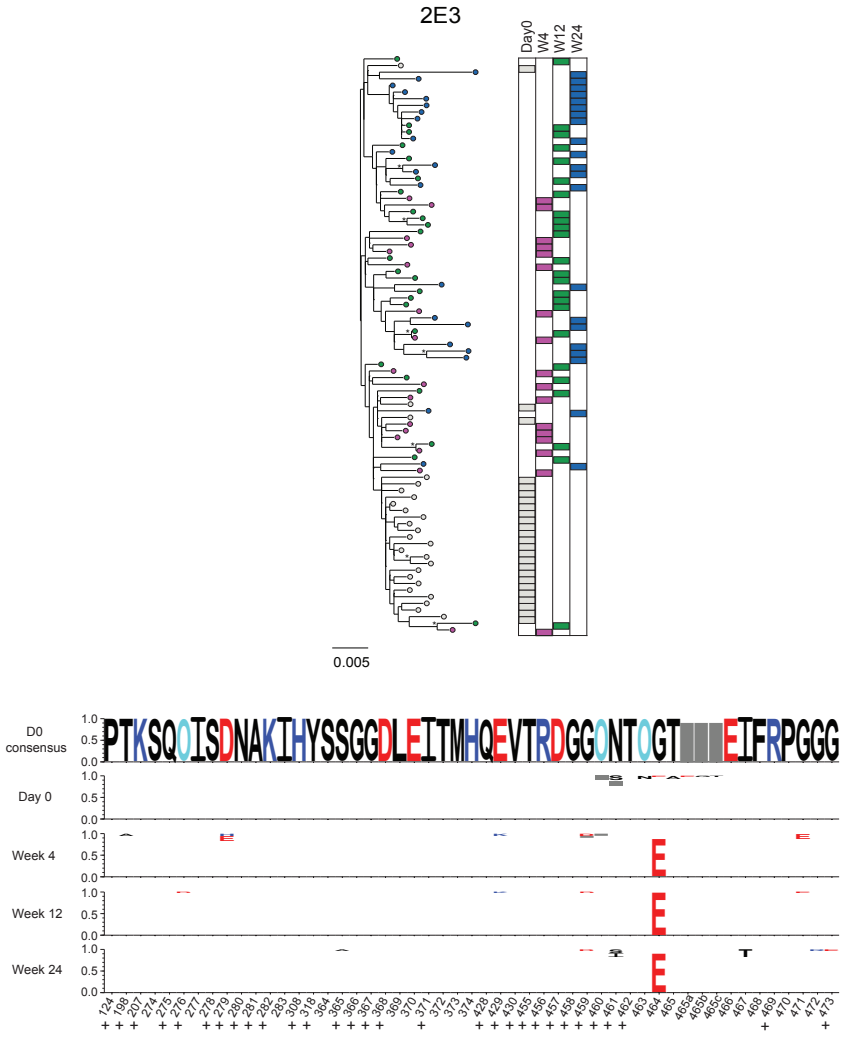

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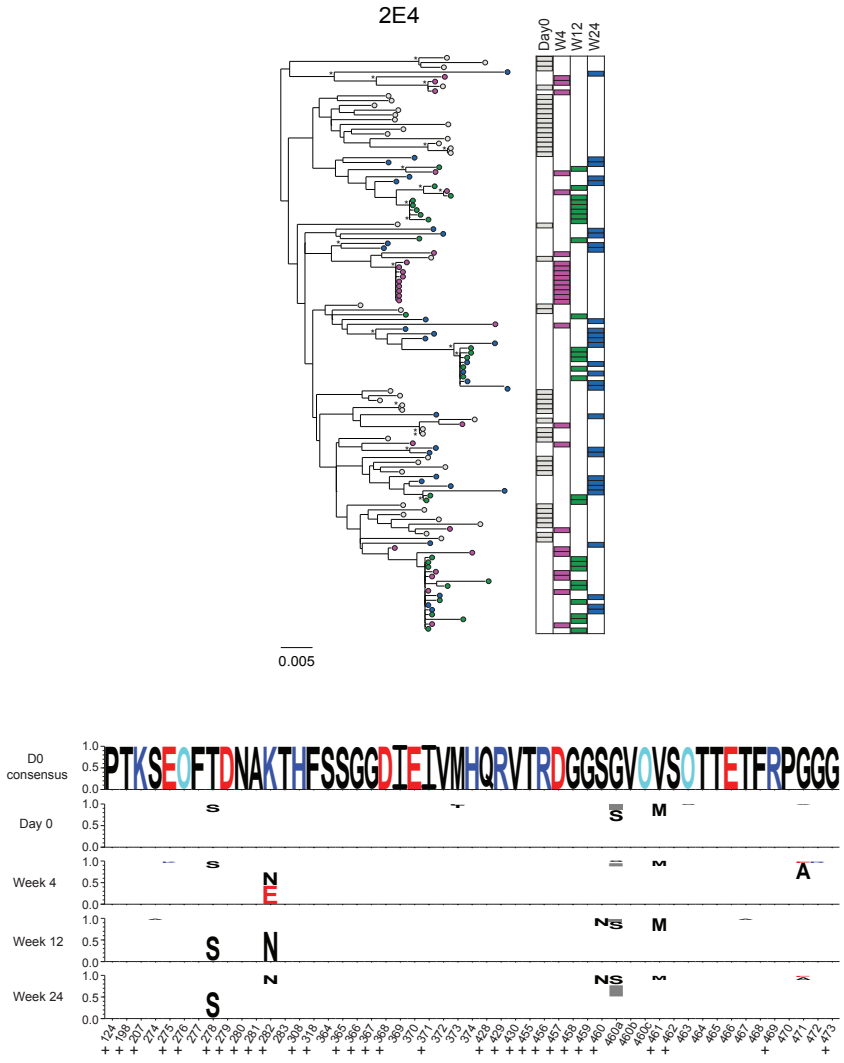

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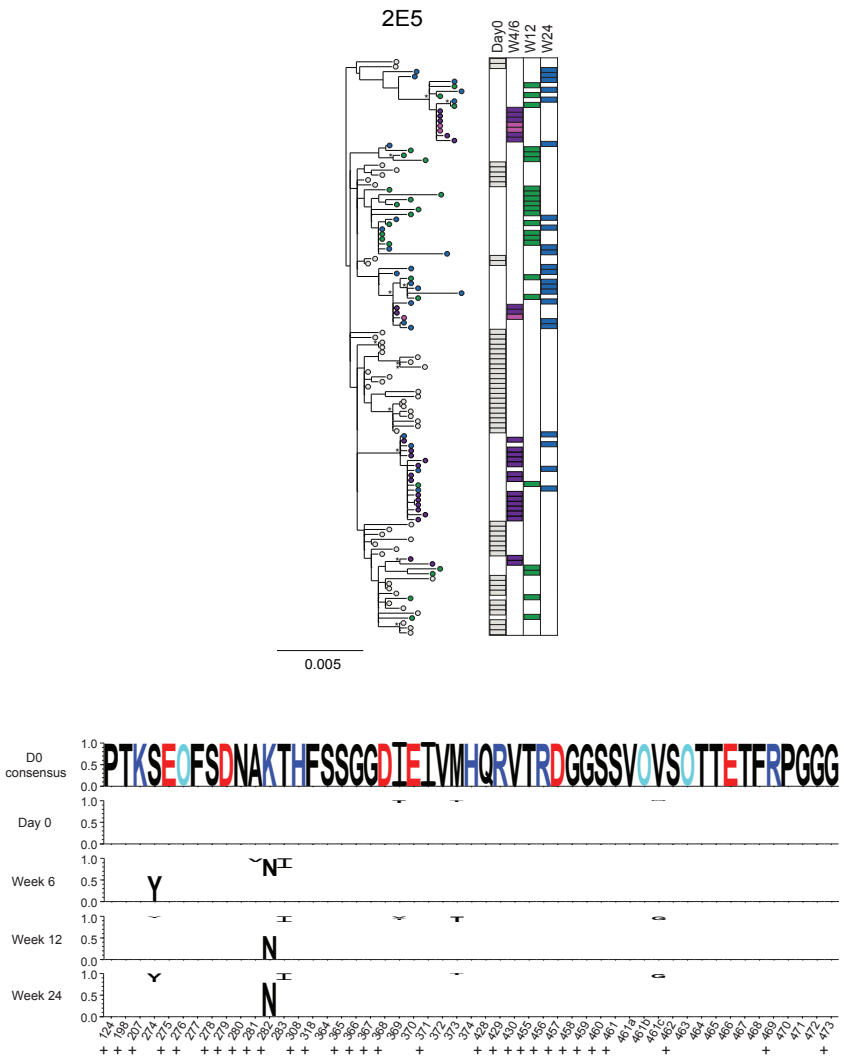

Fig. S7., continued

Viral evolution in subjects 2A3, 2C5, 2C4 and 2E2-2E5. **Top.** Maximum-likelihood phylogenetic trees of plasma-derived env sequences from respective subjects sampled on d0, wk4 (wk6 in case of 2E5), wk12 and wk24 after 3BNC117 infusion. Black asterisks indicate nodes with significant boostrap values (bootstrap support ≥ 70%). Bar graphs (middle) indicate the timepoints from which sequences were derived. For 2E5 pink indicates wk4, dark purple indicates wk6 sequences. **Bottom.** Weblogo plots that illustrate amino acid changes in and directly adjacent to 3BNC117 contact residues over time. White boxes indicate that sequence matches to the d0 consensus, grey boxes indicate gaps in alignment. Colors indicate basic (dark blue) and acidic (red) residues and a turquoise "O" is used instead of "N" to indicate a potential N-glycosylation site. Logo plots were generated using LASSIE (*28*). + symbols indicate contact residues confirmed by two crystal structures (*26, 27*).

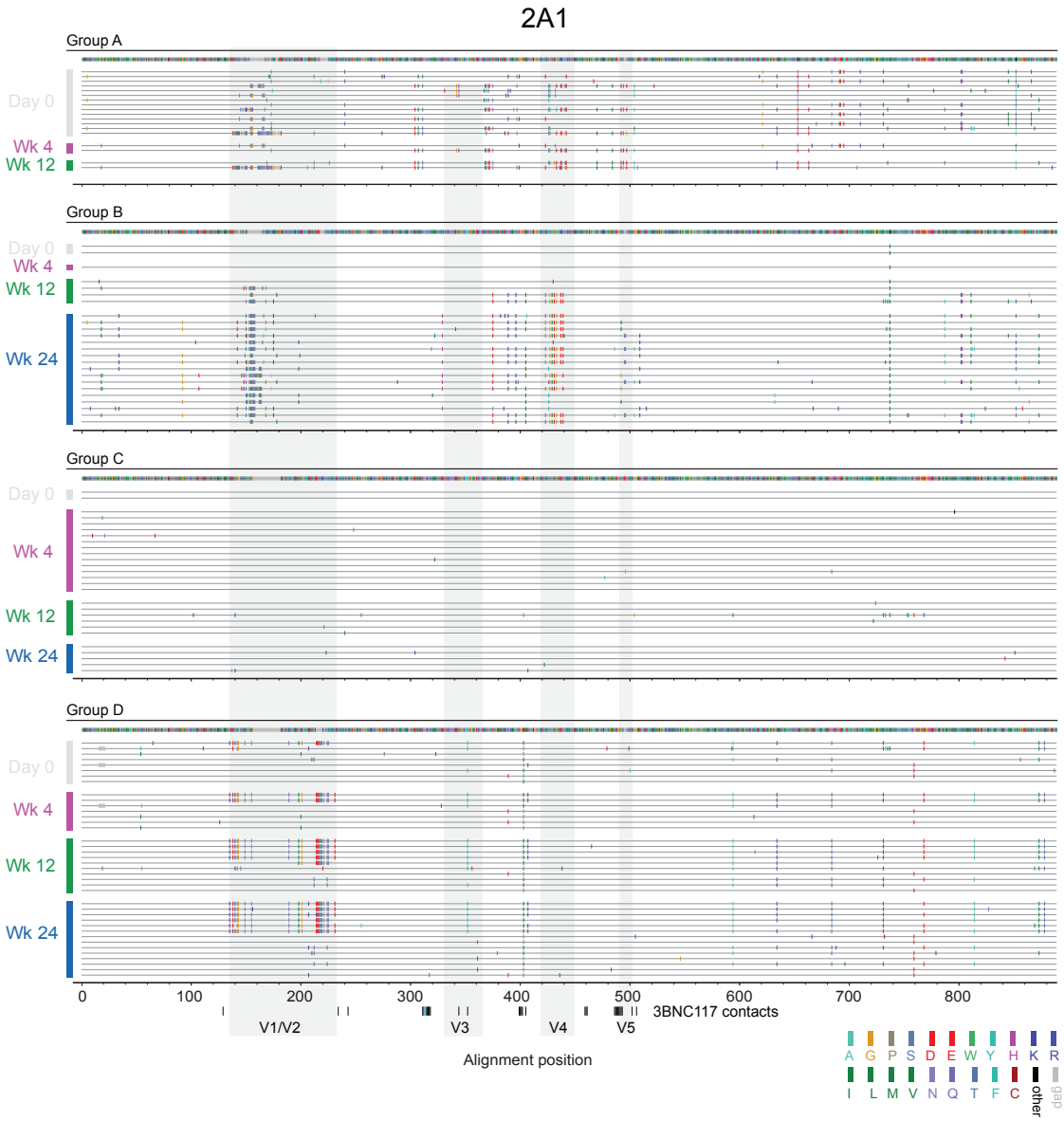

Fig. S8.

Viral sequence evolution in subject 2A1. Amino acid highlighter plots of 2A1 plasma env sequences separated by group (A-D, Fig. 4) illustrate that viral selection in 2A1 occurs mainly by 'clade shifting' with little sequence evolution within 'clades'. Similar patterns of shifting groups of viruses are seen in 2A3 and 2C4 where tree structure is even more complex making clear-cut group analyses challenging. Horizontal lines represent individual sequences and tic marks denote amino acid differences from the respective d0 consensus sequence (cutoff >50% identity) of each group. The amino acid color code key is at the bottom right. Bars to the left indicate the timepoint that each sequence belongs to and is ordered chronologically within each group from top to bottom. Grey-green boxes demarcate variable loops and black/light blue tic marks below the plot indicate 3BNC117 amino acid and glycan contacts, respectively, as determined by two crystal structures (*25, 26*).

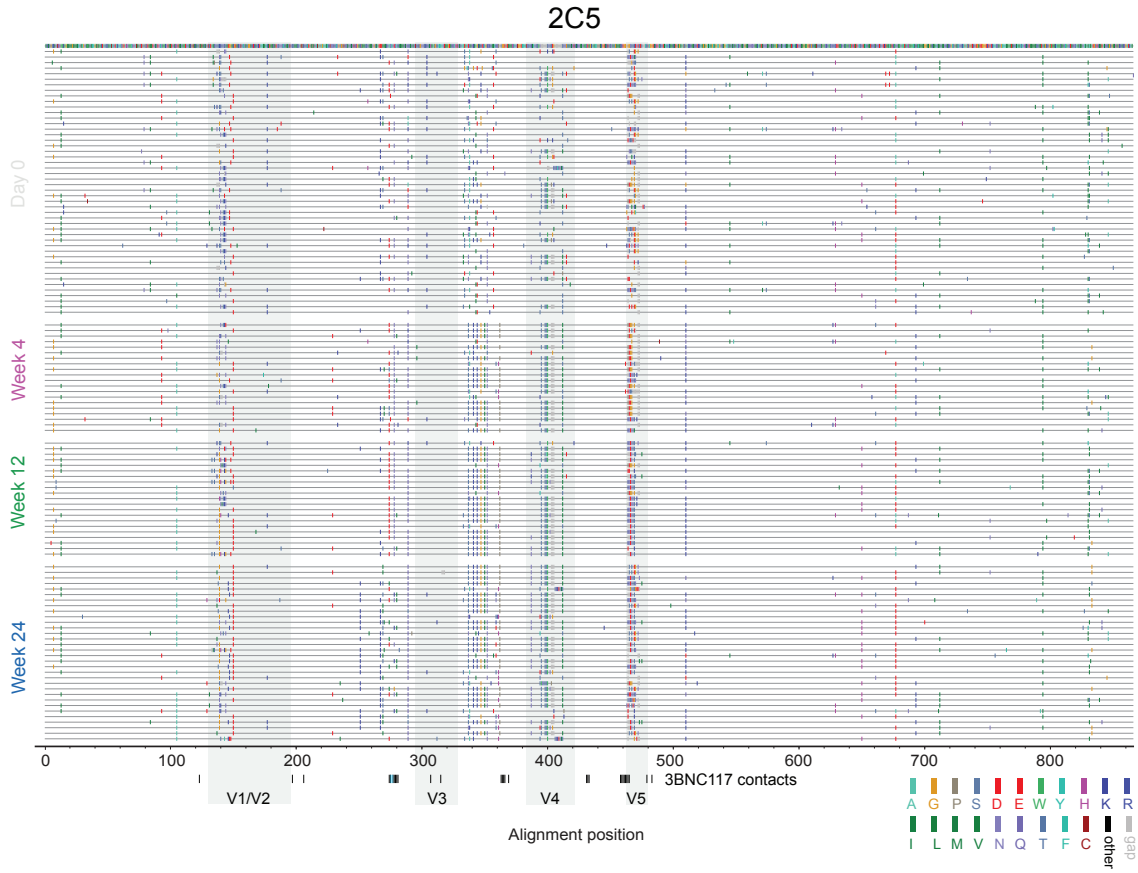

Fig. S9.

Viral sequence evolution in subjects 2C5 and 2E1-2E5. Amino acid highlighter plot for each patient (2C5, 2E1-2E5) depicts sequence changes over time relative to respective d0 consensus (cutoff >50% identity). Horizontal lines represent individual sequences and tic marks denote amino acid differences from consensus sequence. Amino acid color code key is at bottom right. Grey-green boxes demarcate variable loops and black/light blue tic marks underneath plots indicate 3BNC117 amino acid and glycan contacts, respectively, as determined by two crystal structures (*26, 27*). In contrast to subjects 2A1, 2A3 and 2C4, subjects 2C5 and 2E1-2E5 exhibit less complex phylogenies allowing for more stringent calling of a single day0 consensus sequence.

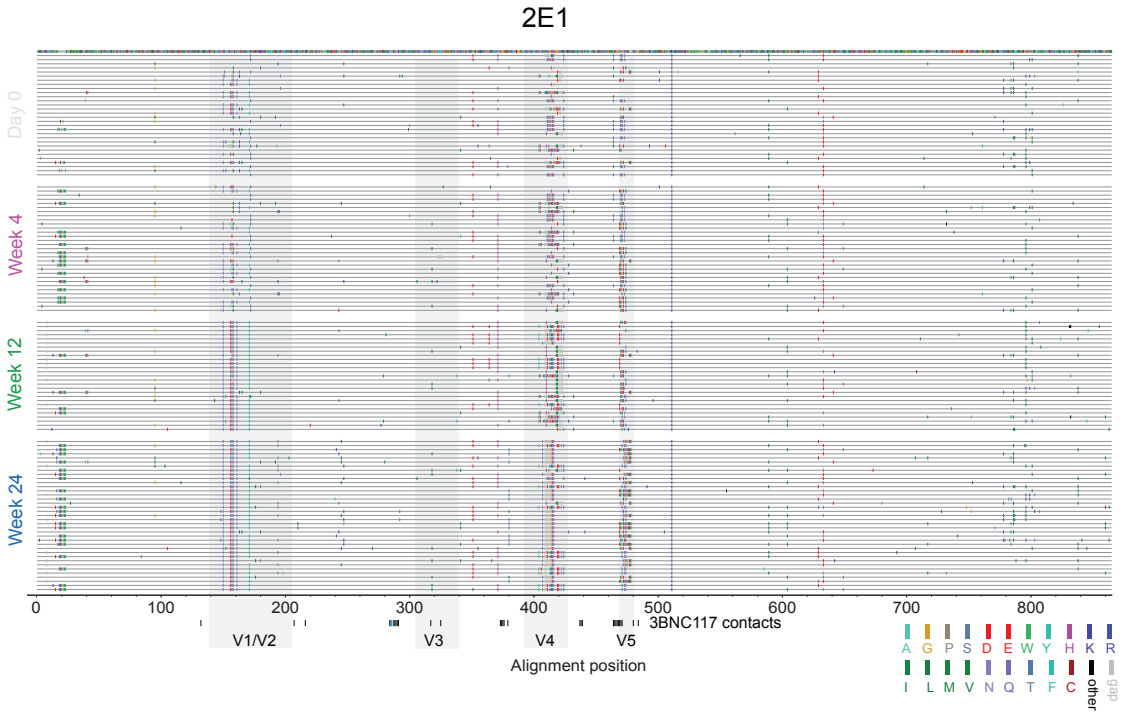

Fig. S9., continued

Viral sequence evolution in subjects 2C5 and 2E1-2E5. Amino acid highlighter plot for each patient (2C5, 2E1-2E5) depicts sequence changes over time relative to respective d0 consensus (cutoff >50% identity). Horizontal lines represent individual sequences and tic marks denote amino acid differences from consensus sequence. Amino acid color code key is at bottom right. Grey-green boxes demarcate variable loops and black/light blue tic marks underneath plots indicate 3BNC117 amino acid and glycan contacts, respectively, as determined by two crystal structures (*26, 27*). In contrast to subjects 2A1, 2A3 and 2C4, subjects 2C5 and 2E1-2E5 exhibit less complex phylogenies allowing for more stringent calling of a single day0 consensus sequence.

2E2

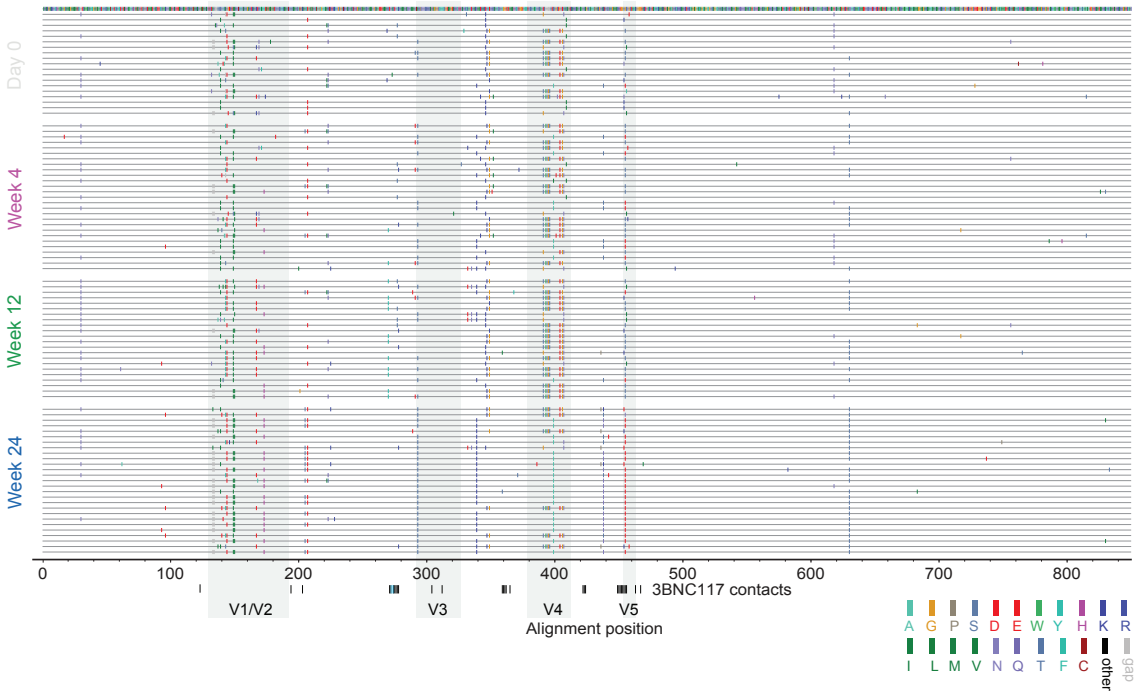

Fig. S9., continued

Viral sequence evolution in subjects 2C5 and 2E1-2E5. Amino acid highlighter plot for each patient (2C5, 2E1-2E5) depicts sequence changes over time relative to respective d0 consensus (cutoff >50% identity). Horizontal lines represent individual sequences and tic marks denote amino acid differences from consensus sequence. Amino acid color code key is at bottom right. Grey-green boxes demarcate variable loops and black/light blue tic marks underneath plots indicate 3BNC117 amino acid and glycan contacts, respectively, as determined by two crystal structures (*26, 27*). In contrast to subjects 2A1, 2A3 and 2C4, subjects 2C5 and 2E1-2E5 exhibit less complex phylogenies allowing for more stringent calling of a single day0 consensus sequence.

2E3

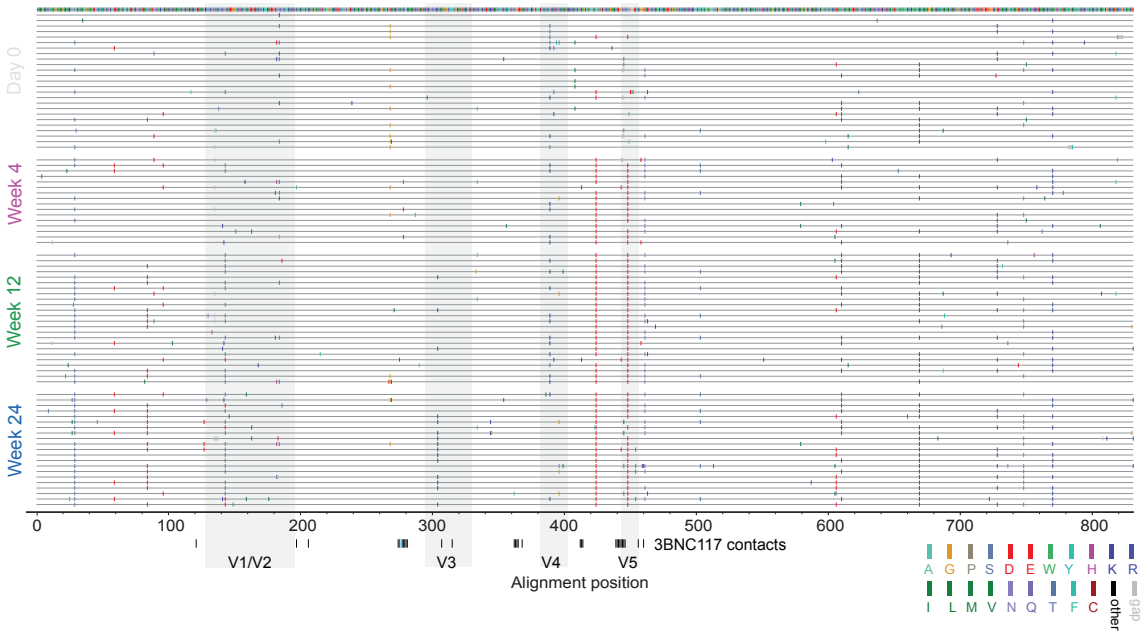

Fig. S9., continued

Viral sequence evolution in subjects 2C5 and 2E1-2E5. Amino acid highlighter plot for each patient (2C5, 2E1-2E5) depicts sequence changes over time relative to respective d0 consensus (cutoff >50% identity). Horizontal lines represent individual sequences and tic marks denote amino acid differences from consensus sequence. Amino acid color code key is at bottom right. Grey-green boxes demarcate variable loops and black/light blue tic marks underneath plots indicate 3BNC117 amino acid and glycan contacts, respectively, as determined by two crystal structures (*26, 27*). In contrast to subjects 2A1, 2A3 and 2C4, subjects 2C5 and 2E1-2E5 exhibit less complex phylogenies allowing for more stringent calling of a single day0 consensus sequence.

2E4

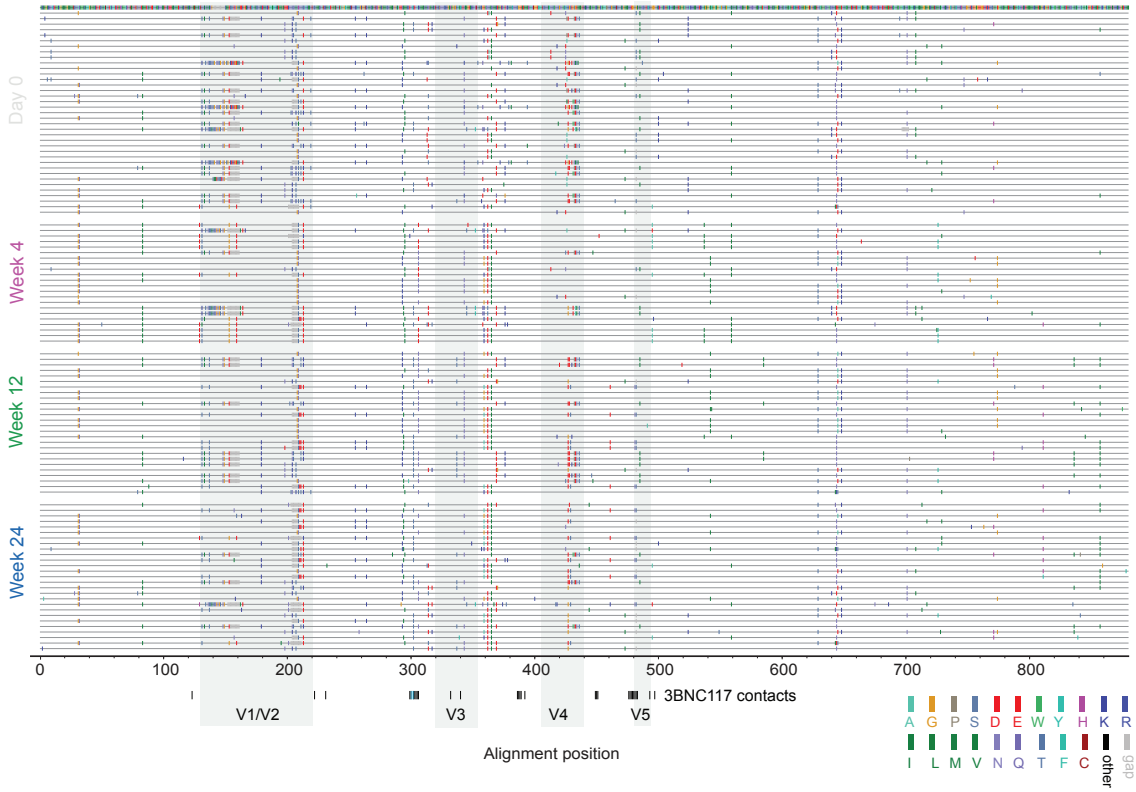

Fig. S9., continued

Viral sequence evolution in subjects 2C5 and 2E1-2E5. Amino acid highlighter plot for each patient (2C5, 2E1-2E5) depicts sequence changes over time relative to respective d0 consensus (cutoff >50% identity). Horizontal lines represent individual sequences and tic marks denote amino acid differences from consensus sequence. Amino acid color code key is at bottom right. Grey-green boxes demarcate variable loops and black/light blue tic marks underneath plots indicate 3BNC117 amino acid and glycan contacts, respectively, as determined by two crystal structures (*26, 27*). In contrast to subjects 2A1, 2A3 and 2C4, subjects 2C5 and 2E1-2E5 exhibit less complex phylogenies allowing for more stringent calling of a single day0 consensus sequence.

2E5

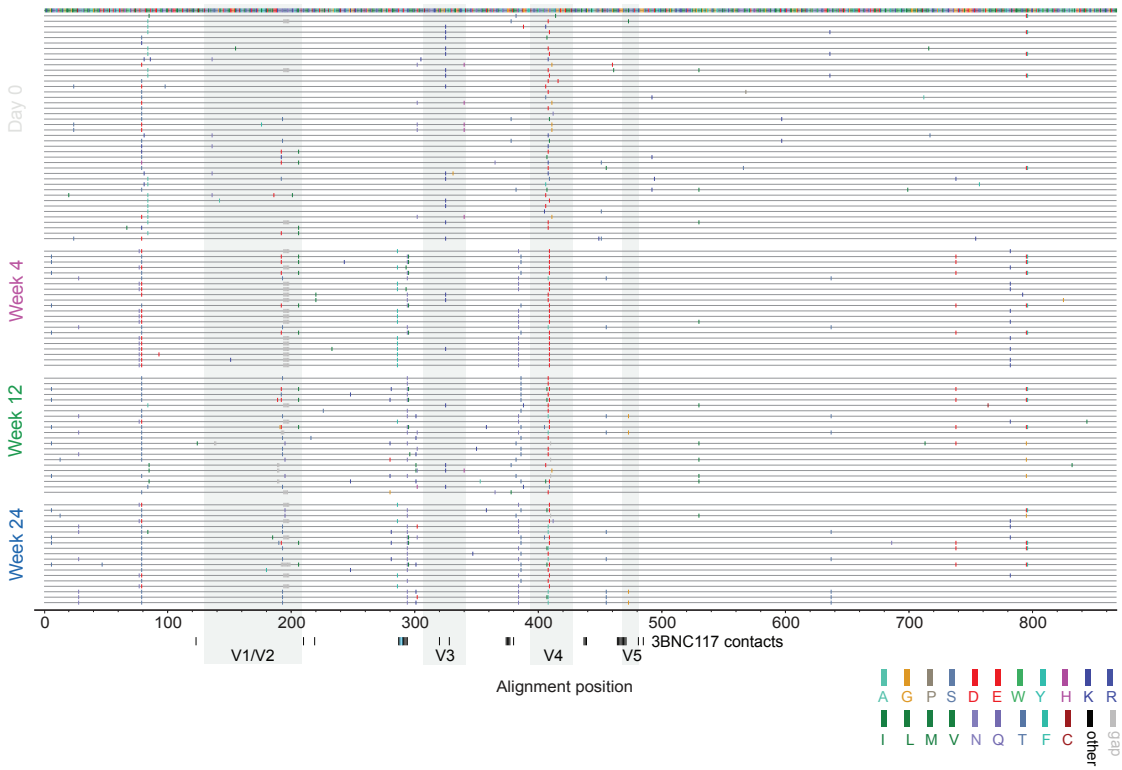

Fig. S9., continued

Viral sequence evolution in subjects 2C5 and 2E1-2E5. Amino acid highlighter plot for each patient (2C5, 2E1-2E5) depicts sequence changes over time relative to respective d0 consensus (cutoff >50% identity). Horizontal lines represent individual sequences and tic marks denote amino acid differences from consensus sequence. Amino acid color code key is at bottom right. Grey-green boxes demarcate variable loops and black/light blue tic marks underneath plots indicate 3BNC117 amino acid and glycan contacts, respectively, as determined by two crystal structures (*26, 27*). In contrast to subjects 2A1, 2A3 and 2C4, subjects 2C5 and 2E1-2E5 exhibit less complex phylogenies allowing for more stringent calling of a single day0 consensus sequence.

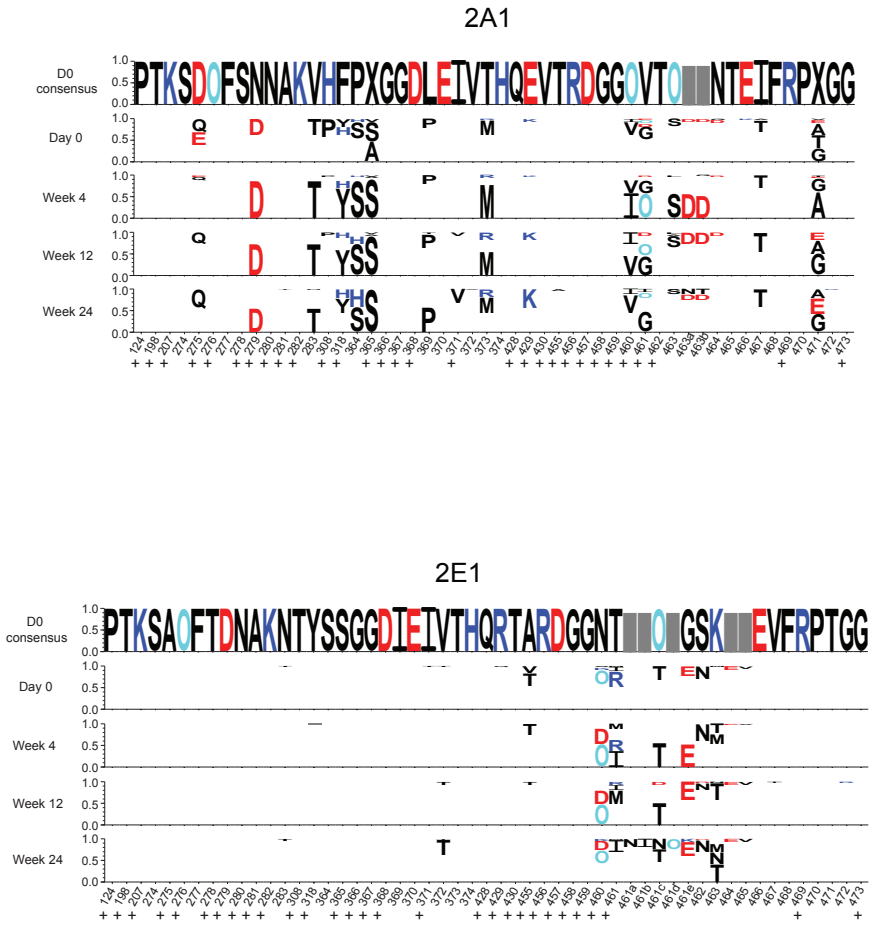

Fig. S10.

Full 3BNC117 contact site logo plots for subjects 2A1 and 2E1. Top. Weblogo plots that illustrate amino acid changes in and directly adjacent to 3BNC117 contact residues over time. White boxes indicate that sequence matches to the d0 consensus, grey boxes indicate gaps in alignment. Colors indicate basic (dark blue) and acidic (red) residues and a turquoise "O" is used instead of "N" to indicate a potential N-glycosylation site. Logo plots were generated using LASSIE (*28*). + symbols indicate 3BNC117 contact residues confirmed by two crystal structures (*26, 27*).

Table S1A.
Clinical characteristics of 3BNC117-treated subjects

Subject ID	3BNC117 dose	Age	Years since HIV Diagnosis	ART regimen pre-therapy	Clade	Sampling Interval (days)	HIV-RNA level (copies/ml)Day 0	HIV-RNA level (copies/ml) Week 24	abs. $CD4^+$ T cell count (day 0; cells/mm^3)	abs. $CD4^+$ T cell count (Week 24; cells/mm^3)
2A1	1 mg/kg	35	11	ART naïve	B	168	3210	2330	674	790
2A3	1 mg/kg	39	14	Off ART	B	171	43650	2870	520	800
2A4	1 mg/kg	42	8	ART naïve	B	167	5340	<20***	607	671
2B1	3 mg/kg	20	1	Off ART	ND	168	4090	<20***	264*	335
2B2	3 mg/kg	48	20	DRV/r/TDF/FTC	ND	167	100	<20	706	578
2B3	3 mg/kg	20	1	ART naïve	B	168	38190	<20***	777	627
2C2	10 mg/kg	51	12	ATV/r/3TC/ZDV	ND	169	30	140	728	804
2C4	10 mg/kg	54	23	Off ART	B	168	820	530	805	821
2C5	10 mg/kg	50	4	ART naïve	B	168	9260	24240	245*	203
2D1	30 mg/kg	33	3	ART naïve	B	168	53470	<20***	980	885
2C1	30 mg/kg	51	17	Off ART	B	168	47650	54950	1129	1026
2D3	30 mg/kg	33	0.5	ART naïve	B	168	640	<20***	618	482
2E1	30 mg/kg	21	2	ART naïve	B	169	15780	16500	847	660
2E2	30 mg/kg	46	1.5	ART naïve	B	169	6990	6590	513	480
2E3	30 mg/kg	23	1.5	ART naïve	BF	168	22030	35200	590	850
2E4	30 mg/kg	38	1	ART naïve	B	169	32220	69300	603	670
2E5	30 mg/kg	30	1	ART naïve	B	169	3610	6110	532	600
5A1	10 mg/kg	28	6	EFV/TDF/FTC	ND	168	<20	<20	814	661
5A2	10 mg/kg	58	19	EFV/TDF/FTC	ND	168	<20	<20	660	619
5A3	10 mg/kg	54	18	EVG/c/FTC/TDF	ND	168	<20	<20	1341	1203
5A4	10 mg/kg	53	5	EFV/TDF/FTC	ND	168	<20	<20	466	574
5A5	10 mg/kg	41	4	EFV/TDF/FTC	ND	168	<20	<20	924	624
5B1	30 mg/kg	58	28	EFV/TDF/FTC	ND	168	<20	<20	654	760
5B2	30 mg/kg	53	19	EFV/ZDV/3TC	ND	168	<20	<20	1065	1053
5B3	30 mg/kg	26	5	EFV/TDF/FTC	ND	168	<20	<20	583	603
5B4	30 mg/kg	64	9	ATV/r/TDF/FTC	ND	168	<20	<20	503	411
5B5	30 mg/kg	63	28	RAL/DRV/r/ETR	ND	168	<20	<20	534	821

* Absolute $CD4^+$ T cell count was 309 and 302 cells/mm^3 at screening. ND - Not Determined

*** Start of ART (Weeks post infusion): 2A3 (24), 2A4 (12), 2B1 (8), 2B3 (12), 2D1 (20), 2D3 (8)

ART-abbreviations: DRV darunavir, TDF tenofovir, FTC emtricitabine, r ritonavir, ATV atazanavir, 3TC lamivudine, ZDV zidovudine, EFV efavirenz, EVG elvitegravir, c cobicistat, RAL raltegravir, ETR etravirine

Table S1B.
Clinical characteristics of untreated viremic subjects

Subject ID	3BNC117 dose	Age	Years since HIV Diagnosis	ART regimen pre-therapy	Clade	Sampling Interval (days)	HIV-RNA level (copies/ml)Day 0	HIV-RNA level (copies/ml) Week 24	abs. $CD4^+$ T cell count (day 0; cells/mm^3)	abs. $CD4^+$ T cell count (Week 24; cells/mm^3)
10518	/	44	24	/	ND	182	38500	10000	643	536
10362	/	56	22	/	ND	190	2380	3670	643	818
10112	/	42	20	/	ND	171	7170	33500	513	551
10962	/	38	11	/	ND	168	7808	14112	489	468
10223	/	44	20	/	ND	196	4590	1300	473	444
10482	/	57	14	/	ND	183	3690	2014	642	640
10210	/	49	16	/	ND	189	3965	31495	546	412
10596	/	43	14	/	ND	188	1607	2269	503	488
10138	/	47	16	/	ND	196	17304	10149	536	532
10108	/	44	18	/	ND	196	7810	37800	850	501
10275	/	36	17	/	ND	181	24600	18220	643	648
10959	/	50	15	/	ND	189	303200	61000	760	621
10367	/	44	20	/	ND	195	432	1460	579	605
10469	/	35	13	/	ND	188	24000	573	1150	682
10410	/	46	4	/	ND	182	42920	62740	522	403
10397	/	39	20	/	ND	182	5327	13520	495	500
10292	/	42	28	/	ND	187	2152	3985	624	642
10802	/	40	2	/	ND	187	150	629	380	302
10099	/	35	12	/	ND	187	9095	12160	669	717
10930	/	52	17	/	ND	188	101500	263700*	562	448*
10417	/	36	5	/	ND	56	16070	41311	328	N/A
10690	/	30	2	/	ND	112	17820	97982	361	N/A
10257	/	32	6	/	ND	196	255	52091	449**	397
10587	/	28	1	/	ND	117	222465	772642	377	N/A
10169	/	34	12	/	ND	617	12423	34836	476	N/A
10160	/	34	0.5	/	ND	106	3984	5495	337	N/A
10811	/	43	20	/	ND	215	2520	5610	307	377
10239	/	46	3	/	ND	245	2660	8659	561	N/A
10814	/	45	5	/	ND	181	45000	33900	567	430
10100	/	37	0.2	/	ND	76	32360	13014	689	N/A
10779	/	33	4	/	ND	89	14029	25234	512	N/A
10785	/	33	1	/	ND	218	7438	148000	550	314
10489	/	41	6	/	ND	169	41100	1750	588	N/A
10082	/	40	9	/	ND	209	37600	104000	469	N/A
10914	/	48	9	/	ND	224	25000	21300	383	N/A
10689	/	28	0.5	/	ND	188	2600	137000	426***	336

* Absolute $CD4^+$ T cell count and HIV-RNA level were measured from a different sample from a timepoint 2 weeks later.

** Absolute $CD4^+$ T cell count was measured from a different sample from a timepoint 2 years earlier. ND - Not Determined. N/A - Not Available

*** Absolute $CD4^+$ T cell count was measured from a different sample from a timepoint 3 months earlier.

Table S2.
Autologous neutralization data of patient IgG against PBMC co-culture virus

		Virus Day 0		Virus Week 4*	
Subject ID	IgG tested	IC_{50} (µg/ml)	AUC	IC_{50} (µg/ml)	AUC
2A1	D0 IgG	>500	0.071	>500	0.11
	w24 IgG	>500	0.209	686.4	0.324
2A3	D0 IgG	>500	**0.571**	>500	0
	w24 IgG	**385.6**	**0.972**	>500	0.115
2C4	D0 IgG	>500	0.203	>500	0.28
	w24 IgG	>500	**0.505**	**286.5**	**0.659**
2C5	D0 IgG	>500	0.354	>500	0.143
	w24 IgG	**287.0**	**1.022**	**226.3**	**0.807**
2E1	D0 IgG	>500	0	>500	0
	w24 IgG	**417.8**	**0.857**	**311.7**	**0.593**
2E2	D0 IgG	>500	0.209	>500	0.319
	w24 IgG	**417.6**	0.401	**194.5**	**0.84**
2E3	D0 IgG	>500	**0.527**	>500	0.308
	w24 IgG	**96.7**	**1.335**	**269.3**	**0.615**
2E4	D0 IgG	>500	0.033	>500	0.005
	w24 IgG	>500	0.038	>500	0.055
2E5	D0 IgG	>500	0.181	>500	0.099
	w24 IgG	**462.6**	0.456	>500	0.253

IgG IC_{50} titers (µg/ml)

0 - 25 µg/ml
25 -100 µg/ml
100 - 400 µg/ml
400 - 500 µg/ml
>500 µg/ml

AUC

> 2
1-2
0.5 - 1
0 - 0.5

* for 2E5 week 6 virus was used instead of week 4

Table S3.
Panel of pseudoviruses used to determine neutralizing activity

HIV-1 Strains	Clade	Tier*
246-F3_C10_2	AC	Tier 2
25710-2.43	C	Tier 2
BaL.26	B	Tier 1B
Ce1176_A3	C	Tier 2
CNE55	AE	Tier 2
CNE8	AE	Tier 2
Q259.d2.17	A	Tier 2
Q769.d22	A	Tier 2
Q842.d12	A	Tier 2
TRO.11	B	Tier 2
X1632_S2_B10	G	Tier 2
YU2.DG	B	Tier 2
ZM135M.PL10a	C	Tier 2

*Tier classification for standard TZM-bl, based on (*21, 43*)

Table S4A.

Heterologous TZM.bl neutralization data of purified patient IgG (IC50 values, µg/ml)

Viremic control patients

Heterologous Strain	Clade	10518 Day 0	10518 Week 26 (182d)	10362 Day 0	10362 Week 27 (190d)	10112 Day 0	10112 Week 24 (171d)	10962 Day 0	10962 Week 24 (168d)	10223 Day 0	10223 Week 28 (196d)
YU2.DG	B	>500	>500	>500	>500	28.7	45.6	69.1	65.2	117.0	130.9
BaL.26	B	43.9	42.8	18.6	19.0	4.4	8.9	9.2	8.1	29.1	26.1
Q769.d22	A1	>500	>500	>500	>500	9.5	23.3	69.4	54.9	75.8	69.8
Q259.d2.17	A1	>500	>500	>500	>500	210.9	233.6	132.0	127.4	232.5	176.5
Q842.d12	A1	>500	>500	>500	>500	10.8	26.7	16.3	17.5	24.4	26.3
ZM135M.PL10a	C	>500	>500	>500	>500	183.1	94.6	233.4	124.8	192.1	490.7
25710-2.43	C	373.9	>500	>500	>500	22.8	42.0	98.7	92.3	79.5	95.6
CNE8	AE	>500	>500	>500	>500	115.4	233.3	163.9	136.4	92.4	84.2
TRO.11	B	>500	>500	>500	>500	19.9	30.0	28.9	27.9	41.1	57.4
X1632_S2_B10	G	>500	>500	>500	>500	>368	>500	258.4	394.5	44.3	70.8
Ce1176_A3	C	>500	>500	>500	>500	28.5	68.7	204.2	161.7	89.8	75.6
246-F3_C10_2	AC	>500	>500	>500	>500	77.4	109.7	278.6	189.5	120.3	123.2
CNE55	AE	>500	>500	>500	>500	*N/A*	196.1	93.1	90.7	34.7	57.1

Heterologous Strain	Clade	10482 Day 0	10482 Week 26 (183d)	10210 Day 0	10210 Week 27 (189d)	10596 Day 0	10596 Week 27 (188d)	10138 Day 0	10138 Week 28 (196d)	10108 Day 0	10108 Week 28 (196d)
YU2.DG	B	>500	>500	384.0	277.2	67.6	83.2	20.9	23.5	54.8	45.6
BaL.26	B	58.9	52.8	19.6	16.5	9.4	8.6	3.4	3.3	1.9	2.1
Q769.d22	A1	>500	>500	>500	>500	>500	>500	38.0	31.4	4.3	5.1
Q259.d2.17	A1	>500	>500	>500	>500	360.2	>500	291.0	371.5	7.2	7.7
Q842.d12	A1	>500	>500	348.5	393.9	89.4	234.6	7.7	11.2	5.2	6.7
ZM135M.PL10a	C	>500	>500	>500	>500	>500	>500	>500	>500	52.5	37.7
25710-2.43	C	>500	>500	480.4	472.1	32.7	61.4	248.2	214.1	14.3	15.1
CNE8	AE	>500	>500	>500	>500	>500	>500	327.4	384.8	27.1	29.9
TRO.11	B	276.6	>500	>500	>500	123.2	91.2	15.0	19.0	5.4	6.4
X1632_S2_B10	G	>500	>500	>500	>500	271.8	228.1	24.2	33.2	6.7	8.6
Ce1176_A3	C	>500	>500	>500	>500	60.3	72.7	>500	>500	94.9	94.1
246-F3_C10_2	AC	>500	>500	>500	>500	>500	>500	193.3	304.6	23.0	22.8
CNE55	AE	>500	>500	>500	>500	>500	>500	189.1	216.5	18.1	21.1

Heterologous Strain	Clade	10275 Day 0	10275 Week 26 (181d)	10959 Day 0	10959 Week 27 (189d)	10367 Day 0	10367 Week 28 (195d)	10469 Day 0	10469 Week 27 (188d)	10410 Day 0	10410 Week 26 (182d)
YU2.DG	B	>500	>500	41.8	41.6	24.8	22.0	439.4	431.5	>500	>500
BaL.26	B	27.1	34.2	10.7	11.8	5.0	6.0	26.4	35.6	56.0	32.0
Q769.d22	A1	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
Q259.d2.17	A1	>500	>500	>500	>500	166.5	222.0	89.9	139.0	>500	>500
Q842.d12	A1	>500	>500	16.3	17.8	170.9	>500	295.7	373.6	>500	>500
ZM135M.PL10a	C	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
25710-2.43	C	>500	>500	320.5	334.3	23.7	24.1	302.2	273.4	>500	276.4
CNE8	AE	>500	>500	493.4	428.4	>500	>500	>500	>500	>500	>500
TRO.11	B	>500	>500	51.1	45.2	11.3	10.5	>500	>500	>500	>500
X1632_S2_B10	G	>500	>500	136.9	105.6	102.5	90.4	>500	>500	>500	>500
Ce1176_A3	C	>500	>500	>500	>500	20.4	21.6	>500	>500	>500	>500
246-F3_C10_2	AC	>500	>500	227.2	209.5	36.8	46.0	>500	>500	>500	>500
CNE55	AE	>500	>500	51.0	60.9	>500	>500	>500	>500	>500	>500

Heterologous Strain	Clade	10397 Day 0	10397 Week 26 (182d)	10292 Day 0	10292 Week 27 (187d)	10802 Day 0	10802 Week 27 (187d)
YU2.DG	B	160.4	133.8	298.1	279.9	>500	>500
BaL.26	B	7.4	8.0	17.7	21.1	>500	>500
Q769.d22	A1	>500	>500	>500	>500	>500	>500
Q259.d2.17	A1	>500	>500	>500	>500	>500	>500
Q842.d12	A1	>500	438.3	313.0	273.4	>500	>500
ZM135M.PL10a	C	>500	>500	>500	>500	>500	>500
25710-2.43	C	182.4	320.5	429.6	445.7	>500	>500
CNE8	AE	>500	>500	378.7	485.3	>500	>500
TRO.11	B	422.6	422.4	482.1	>500	>500	>500
X1632_S2_B10	G	>500	>500	>500	>500	>500	>500
Ce1176_A3	C	>500	>500	>500	>500	56.4	61.9
246-F3_C10_2	AC	>500	>500	>500	>500	>500	>500
CNE55	AE	>500	>500	>500	>500	>500	>500

IgG IC_{50} titers (ug/ml)

0 - 25 µg/ml

25 -100 µg/ml

100 - 400 µg/ml

400 - 500 µg/ml

>500 µg/ml

Table S4A.

Heterologous TZM.bl neutralization data of purified patient IgG (IC50 values, µg/ml), continued

Heterologous Strain	Clade	10099 Day 0	10099 Week 27 (187d)	10930 Day 0	10930 Week 27 (188d)	10417 Day 0	10417 Week 8 (56d)	10690 Day 0	10690 Week 16 (112d)	10257 Day 0	10257 Week 28 (196d)
YU2.DG	B	>500	>500	102.2	122.5	405.2	>500	95.2	92.9	211.3	169.4
BaL.26	B	52.3	42.1	15.8	16.8	6.4	5.5	24.2	33.4	25.7	26.2
Q769.d22	A1	>500	>500	204.5	343.0	>500	>500	>500	>500	>500	>500
Q259.d2.17	A1	>500	>500	199.1	250.1	>500	>500	>500	>500	295.5	183.0
Q842.d12	A1	>500	>500	61.8	77.1	333.4	301.8	455.4	366.8	136.0	70.2
ZM135M.PL10a	C	>500	>500	>500	>500	219.6	133.7	>500	>500	254.0	155.6
25710-2.43	C	432.6	244.7	235.7	326.7	161.8	90.7	226.9	202.7	169.4	94.1
CNE8	AE	443.1	>500	29.6	39.2	48.5	32.9	365.6	295.1	150.2	117.5
TRO.11	B	187.5	198.6	81.9	122.4	81.7	68.8	174.4	166.6	67.7	62.2
X1632_S2_B10	G	>500	>500	54.4	109.2	>500	>500	228.0	122.1	369.1	175.5
Ce1176_A3	C	>500	>500	340.1	405.1	367.7	445.0	363.8	347.3	>500	>500
246-F3_C10_2	AC	>500	>500	56.4	61.9	>500	>500	>500	>500	>500	>500
CNE55	AE	>500	>500	87.7	83.6	476.1	453.9	>500	>500	>500	>500

Heterologous Strain	Clade	10587 Day 0	10587 Week 17 (117d)	10169 Day 0	10169 Week 88 (617d)	10160 Day 0	10160 Week 15 (106d)	10811 Day 0	10811 Week 31 (215d)	10239 Day 0	10239 Week 35 (245d)
YU2.DG	B	>500	>500	29.2	49.5	267.5	396.7	325.0	389.9	>500	>500
BaL.26	B	44.4	50.8	4.7	6.4	28.4	28.2	80.0	71.8	55.2	75.7
Q769.d22	A1	140.5	276.7	25.2	39.9	>500	>500	>500	498.6	>500	>500
Q259.d2.17	A1	>500	>500	72.2	102.9	>500	>500	>500	>500	>500	>500
Q842.d12	A1	252.5	194.6	21.2	33.5	>500	>500	476.7	146.2	>500	>500
ZM135M.PL10a	C	>500	>500	67.4	163.2	>500	>500	>500	>500	>500	>500
25710-2.43	C	377.1	416.7	74.2	37.1	199.7	300.0	254.5	84.6	245.7	326.5
CNE8	AE	>500	>500	45.7	67.3	>500	>500	>500	>500	>500	>500
TRO.11	B	66.0	102.2	13.9	16.1	52.4	72.5	294.6	71.8	>500	>500
X1632_S2_B10	G	>500	>500	68.2	41.3	>500	>500	>500	>500	>500	>500
Ce1176_A3	C	>500	448.5	96.3	150.0	301.2	438.5	426.7	117.2	>500	>500
246-F3_C10_2	AC	>500	>500	122.8	245.4	>500	>500	>500	278.4	>500	>500
CNE55	AE	>500	311.7	75.2	100.2	>500	>500	472.9	255.5	>500	>500

Heterologous Strain	Clade	10814 Day 0	10814 Week 26 (181d)	10100 Day 0	10100 Week 11 (76d)	10779 Day 0	10779 Week 13 (89d)	10785 Day 0	10785 Week 31 (218d)	10489 Day 0	10489 Week 24 (169d)
YU2.DG	B	>500	>500	>500	>500	>500	>500	>500	>500	221.2	239.7
BaL.26	B	126.4	180.7	77.5	96.4	35.0	26.8	23.4	24.6	13.8	20.9
Q769.d22	A1	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
Q259.d2.17	A1	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
Q842.d12	A1	>500	>500	>500	>500	>500	>500	473.0	>500	>500	>500
ZM135M.PL10a	C	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
25710-2.43	C	>500	>500	>500	>500	>500	>500	149.9	151.3	399.0	360.7
CNE8	AE	228.4	233.6	>500	>500	205.3	310.0	>500	>500	>500	>500
TRO.11	B	134.6	175.1	>500	>500	>500	>500	>500	>500	59.2	73.2
X1632_S2_B10	G	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
Ce1176_A3	C	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
246-F3_C10_2	AC	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
CNE55	AE	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500

Heterologous Strain	Clade	10082 Day 0	10082 Week 30 (209d)	10914 Day 0	10914 Week 32 (224d)	10689 Day 0	10689 Week 27 (188d)
YU2.DG	B	>500	>500	170.5	>500	>500	>500
BaL.26	B	34.2	38.8	29.7	77.8	29.0	43.2
Q769.d22	A1	>500	>500	>500	>500	>500	>500
Q259.d2.17	A1	>500	>500	>500	>500	>500	>500
Q842.d12	A1	>500	>500	>500	>500	>500	>500
ZM135M.PL10a	C	>500	>500	209.9	419.4	>500	>500
25710-2.43	C	>500	>500	213.9	456.7	488.1	419.1
CNE8	AE	>500	>500	276.4	>500	>500	>500
TRO.11	B	487.1	>500	307.7	>500	>500	>500
X1632_S2_B10	G	>500	>500	>500	>500	>500	>500
Ce1176_A3	C	>500	>500	329.3	>500	>500	>500
246-F3_C10_2	AC	>500	>500	>500	>500	>500	>500
CNE55	AE	>500	>500	>500	>500	>500	>500

IgG IC_{50} titers (ug/ml)

0 - 25 µg/ml

25 -100 µg/ml

100 - 400 µg/ml

400 - 500 µg/ml

>500 µg/ml

Table S4A.

Heterologous TZM.bl neutralization data of purified patient IgG (IC50 values, µg/ml), continued
3BNC117-treated viremic patients

Heterologous Strain	Clade	2A1		2A3		2A4		2B1		2B3	
		Day -7	Week 24	Day 0	Week 24	Day -7	Week 24	Day -7	Week 24	Day -7	Week 24
YU2.DG	B	**24.9**	**22.2**	>500	**363.4**	>500	>500	>500	>500	>500	>500
BaL.26	B	**3.3**	**3.2**	**28.4**	**18.9**	**89.5**	**71.3**	**135.0**	**164.8**	**365.9**	**310.8**
Q769.d22	A1	**102.6**	**97.0**	>500	**19.4**	>500	>500	>500	>500	>500	>500
Q259.d2.17	A1	**170.9**	**70.4**	**92.5**	**84.7**	>500	>500	>500	>500	>500	>500
Q842.d12	A1	**22.2**	**18.3**	**475.0**	**417.8**	>500	>500	>500	>500	>500	>500
ZM135M.PL10a	C	>500	**234.5**	>500	>500	>500	>500	>500	>500	>500	>500
25710-2.43	C	>500	**324.1**	**110.8**	**136.0**	>500	>500	>500	>500	>500	>500
CNE8	AE	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
TRO.11	B	**137.7**	**52.9**	**218.6**	**203.0**	>500	>500	>500	>500	>500	**495.5**
X1632_S2_B10	G	**65.1**	**48.3**	>500	>500	>500	>500	>500	>500	>500	>500
Ce1176_A3	C	>500	>500	**482.2**	**446.7**	>500	>500	>500	>500	>500	>500
246-F3_C10_2	AC	*N/A*	**297.2**	**445.4**	**283.7**	*N/A*	>500	*N/A*	>500	*N/A*	>500
CNE55	AE	>500	**204.8**	>500	>500	>500	>500	>500	>500	>500	>500

Heterologous Strain	Clade	2C4		2C5		2D1		2C1		2D3	
		Day -7	Week 24	Day -7	Week 24	Day 0	Week 24	Day -7	Week 24	Day -7	Week24
YU2.DG	B	**120.6**	**69.8**	>500	>500	>500	>500	>500	>500	>500	>500
BaL.26	B	**43.0**	**15.7**	**40.2**	**15.1**	**114.6**	**69.4**	**111.2**	**51.1**	>500	>500
Q769.d22	A1	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
Q259.d2.17	A1	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
Q842.d12	A1	**82.0**	**86.7**	>500	>500	>500	>500	>500	**423.1**	>500	**369.1**
ZM135M.PL10a	C	>500	**419.5**	>500	**225.8**	>500	>500	>500	>500	>500	>500
25710-2.43	C	**241.8**	**49.6**	**305.9**	**159.6**	>500	>500	**426.3**	**125.4**	>500	>500
CNE8	AE	**325.3**	**83.3**	>500	**240.4**	>500	>500	>500	>500	>500	>500
TRO.11	B	**69.8**	**13.3**	>500	**316.7**	>500	>500	>500	**486.2**	>500	>500
X1632_S2_B10	G	>500	**378.2**	>500	>500	>500	>500	>500	>500	>500	>500
Ce1176_A3	C	>500	**79.0**	>500	>500	>500	>500	>500	>500	>500	>500
246-F3_C10_2	AC	*N/A*	**190.1**	*N/A*	>500	>500	>500	*N/A*	>500	>500	>500
CNE55	AE	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500

Heterologous Strain	Clade	2E1		2E2		2E3		2E4		2E5	
		Day 0	Week 24	Day 0	Week 24	Day 0	Week 24	Day 0	Week 24	Day 0	Week 24
YU2.DG	B	>500	>500	>500	>500	>500	>500	>500	**495.7**	>500	>500
BaL.26	B	**87.4**	**41.1**	**28.9**	**16.8**	**85.2**	**24.2**	**103.0**	**87.7**	**393.8**	**66.1**
Q769.d22	A1	**407.3**	**181.7**	>500	>500	>500	>500	>500	>500	>500	>500
Q259.d2.17	A1	>500	>500	>500	>500	>500	>500	>500	**366.6**	>500	**480.4**
Q842.d12	A1	>500	>500	>500	>500	>500	>500	**467.2**	**333.4**	>500	**463.1**
ZM135M.PL10a	C	>500	>500	>500	>500	>500	>500	**366.3**	**495.1**	>500	>500
25710-2.43	C	**439.1**	**397.9**	>500	>500	>500	**471.6**	**148.4**	**158.7**	>500	>500
CNE8	AE	>500	>500	>500	>500	>500	>500	**177.8**	**98.5**	>500	>500
TRO.11	B	**483.4**	**135.8**	>500	>500	>500	>500	**188.4**	**193.4**	>500	>500
X1632_S2_B10	G	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
Ce1176_A3	C	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
246-F3_C10_2	AC	>500	>500	>500	>500	>500	>500	**277.1**	**483.5**	>500	>500
CNE55	AE	>500	>500	NT	>500	>500	>500	>500	>500	>500	>500

IgG IC_{50} titers (ug/ml)
0 - 25 µg/ml
25 -100 µg/mll
100 - 400 µg/ml
400 - 500 µg/ml
>500 µg/ml

Table S4A.
Heterologous TZM.bl neutralization data of purified patient IgG (IC50 values, µg/ml), continued

3BNC117-treated patients on-ART

Heterologous Strain	Clade	5A1		5A2		5A3		5A4		5A5	
		Day 0	Week 24	Day 0	Week 24	Day 0	Week 24	Day 0	Week 24	Day 0	Week 24
YU2.DG	B	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
BaL.26	B	>500	>500	**155.0**	**177.1**	**83.9**	**27.3**	>500	**404.5**	>500	>500
Q769.d22	A1	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
Q259.d2.17	A1	>500	>500	>500	>500	>500	**430.6**	>500	>500	>500	>500
Q842.d12	A1	>500	>500	>500	>500	>500	**388.4**	>500	**492.9**	>500	>500
ZM135M.PL10a	C	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
25710-2.43	C	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
CNE8	AE	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
TRO.11	B	>500	>500	>500	>500	>500	**416.3**	>500	>500	>500	>500
X1632_S2_B10	G	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
Ce1176_A3	C	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
246-F3_C10_2	AC	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
CNE55	AE	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500

Heterologous Strain	Clade	5B1		5B2		5B3		5B4		5B5	
		Day 0	Week 24	Day 0	Week 24	Day 0	Week 24	Day 0	Week 24	Day 0	Week 24
YU2.DG	B	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
BaL.26	B	**129.2**	**134.1**	**127.9**	**152.5**	>500	>500	**66.8**	**46.4**	**124.8**	**89.5**
Q769.d22	A1	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
Q259.d2.17	A1	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
Q842.d12	A1	>500	>500	>500	**435.0**	>500	>500	>500	>500	**359.3**	**298.1**
ZM135M.PL10a	C	>500	>500	>500	>500	>500	>500	>500	>500	>500	**460.0**
25710-2.43	C	>500	>500	>500	>500	>500	>500	>500	>500	**497.9**	**497.9**
CNE8	AE	>500	>500	>500	>500	>500	>500	>500	>500	>500	**219.8**
TRO.11	B	>500	>500	>500	>500	>500	>500	>500	>500	>500	**487.3**
X1632_S2_B10	G	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
Ce1176_A3	C	>500	>500	>500	>500	>500	>500	>500	>500	>500	>500
246-F3_C10_2	AC	>500	>500	>500	>500	>500	>500	>500	>500	>500	**279.2**
CNE55	AE	>500	>500	>500	>500	>500	>500	>500	>500	>500	**381.2**

Heterologous Strain	Clade	2B2		2C2	
		Day -7	Week 24	Day -7	Week 24
YU2.DG	B	>500	>500	>500	>500
BaL.26	B	**237.0**	**231.1**	**134.3**	**75.8**
Q769.d22	A1	>500	>500	>500	>500
Q259.d2.17	A1	>500	>500	>500	>500
Q842.d12	A1	>500	>500	>500	>500
ZM135M.PL10a	C	>500	>500	>500	>500
25710-2.43	C	>500	>500	>500	>500
CNE8	AE	>500	>500	>500	>500
TRO.11	B	>500	>500	>500	**353.6**
X1632_S2_B10	G	>500	>500	>500	>500
Ce1176_A3	C	>500	>500	>500	>500
246-F3_C10_2	AC	*N/A*	>500	*N/A*	>500
CNE55	AE	>500	>500	>500	>500

IgG IC_{50} titers (ug/ml)

0 - 25 µg/ml

25 -100 µg/ml

100 - 400 µg/ml

400 - 500 µg/ml

>500 µg/ml

Table S4B.
Heterologous TZM.bl neutralization data of purified patient IgG (AUC)
Viremic control patients

Heterologous Strain	Clade	10518 Day 0	10518 Week 26 (182d)	10362 Day 0	10362 Week 27 (190d)	10112 Day 0	10112 Week 24 (171d)	10962 Day 0	10962 Week 24 (168d)	10223 Day 0	10223 Week 28 (196d)
YU2.DG	B	0.24	0.18	0.09	0.13	**2.08**	**1.90**	**1.43**	**1.51**	**1.13**	**1.09**
BaL.26	B	**1.79**	**1.96**	**2.61**	**2.64**	**3.30**	**3.08**	**3.13**	**3.19**	**2.39**	**2.36**
Q769.d22	A1	0.17	0.40	0.37	0.24	**2.70**	**2.49**	**1.57**	**1.60**	**1.52**	**1.41**
Q259.d2.17	A1	0.03	0.19	0.05	0.07	**0.73**	**0.71**	**1.11**	**1.06**	**0.79**	**0.87**
Q842.d12	A1	0.31	0.27	0.16	**0.51**	**2.77**	**2.44**	**2.80**	**2.70**	**2.52**	**2.49**
ZM135M.PL10a	C	0.02	0.31	0.05	0.13	**0.87**	**1.31**	**0.79**	**1.28**	**0.93**	**0.71**
25710-2.43	C	**0.76**	**0.52**	0.32	0.29	**2.32**	**1.98**	**1.18**	**1.36**	**1.36**	**1.34**
CNE8	AE	0.00	0.00	0.00	0.04	**1.01**	**0.66**	**0.88**	**1.04**	**1.43**	**1.47**
TRO.11	B	0.09	0.43	0.23	0.22	**2.33**	**2.29**	**2.32**	**2.21**	**2.01**	**1.70**
X1632_S2_B10	G	0.32	**0.75**	**0.58**	0.15	0.39	**0.64**	**1.09**	**0.91**	**1.98**	**1.61**
Ce1176_A3	C	0.21	0.09	0.35	0.07	**1.94**	**1.65**	**0.84**	**0.99**	**1.43**	**1.58**
246-F3_C10_2	AC	0.00	0.04	0.03	0.09	**1.27**	**1.16**	**0.83**	**0.81**	**1.12**	**1.15**
CNE55	AE	0.00	0.23	0.26	0.00	*N/A*	*N/A*	**1.41**	**1.31**	**2.13**	**1.68**

Heterologous Strain	Clade	10482 Day 0	10482 Week 26 (183d)	10210 Day 0	10210 Week 27 (189d)	10596 Day 0	10596 Week 27 (188d)	10138 Day 0	10138 Week 28 (196d)	10108 Day 0	10108 Week 28 (196d)
YU2.DG	B	0.06	0.09	**0.51**	**0.64**	**1.51**	**1.46**	**2.64**	**2.55**	**1.73**	**1.84**
BaL.26	B	**1.75**	**1.75**	**2.54**	**2.78**	**3.09**	**3.08**	**3.59**	**3.54**	**3.75**	**3.69**
Q769.d22	A1	0.29	**0.63**	0.41	0.08	0.34	0.25	**1.90**	**1.83**	**3.46**	**3.36**
Q259.d2.17	A1	0.18	0.18	0.40	0.26	**0.71**	0.23	**0.66**	**0.68**	**3.28**	**3.26**
Q842.d12	A1	**0.59**	0.49	**0.90**	**0.89**	**1.40**	**1.03**	**3.20**	**3.03**	**3.38**	**3.19**
ZM135M.PL10a	C	0.13	0.09	0.38	0.46	**0.73**	0.36	**0.68**	**0.83**	**1.85**	**1.92**
25710-2.43	C	**0.54**	**0.72**	0.46	**0.58**	**2.20**	**1.71**	**0.81**	**0.79**	**2.74**	**2.72**
CNE8	AE	0.04	0.06	0.00	0.04	0.10	0.07	0.48	0.40	**2.34**	**2.26**
TRO.11	B	**0.93**	**0.95**	**0.73**	**0.58**	**1.20**	**1.47**	**2.70**	**2.54**	**3.38**	**3.27**
X1632_S2_B10	G	0.20	0.02	0.36	0.08	**0.73**	**1.13**	**2.32**	**2.16**	**3.21**	**3.12**
Ce1176_A3	C	0.31	0.24	**0.59**	0.35	**1.76**	**1.53**	0.15	0.34	**1.28**	**1.46**
246-F3_C10_2	AC	0.14	0.13	0.19	0.19	0.49	0.19	**0.92**	**0.65**	**2.54**	**2.53**
CNE55	AE	0.14	0.15	0.28	0.05	0.00	0.00	**1.19**	**1.01**	**2.68**	**2.50**

Heterologous Strain	Clade	10275 Day 0	10275 Week 26 (181d)	10959 Day 0	10959 Week 27 (189d)	10367 Day 0	10367 Week 28 (195d)	10469 Day 0	10469 Week 27 (188d)	10410 Day 0	10410 Week 26 (182d)
YU2.DG	B	0.05	0.16	**2.02**	**2.04**	**2.50**	**2.58**	**0.66**	**0.72**	0.21	0.13
BaL.26	B	**2.32**	**2.19**	**3.02**	**2.99**	**3.38**	**3.37**	**2.32**	**2.16**	**1.69**	**2.24**
Q769.d22	A1	0.10	0.40	0.40	0.45	0.35	0.23	0.31	0.47	0.00	0.00
Q259.d2.17	A1	0.14	0.09	0.23	0.21	**0.93**	**0.74**	**1.35**	**1.03**	0.00	0.01
Q842.d12	A1	0.41	**0.55**	**2.83**	**2.76**	**1.16**	**0.55**	**0.71**	**0.73**	0.49	0.33
ZM135M.PL10a	C	0.35	0.48	0.38	0.31	**0.78**	0.34	0.21	0.12	0.21	0.18
25710-2.43	C	0.46	0.40	**0.58**	**0.57**	**2.48**	**2.46**	**0.86**	**0.97**	0.41	**1.08**
CNE8	AE	0.02	0.00	0.23	0.34	0.14	0.22	0.08	0.08	0.00	0.00
TRO.11	B	0.24	0.27	**1.83**	**1.86**	**3.03**	**3.07**	**0.92**	**0.82**	0.00	0.03
X1632_S2_B10	G	0.20	0.22	**1.07**	**1.19**	**1.26**	**1.41**	**0.69**	**0.65**	0.29	0.23
Ce1176_A3	C	0.44	**0.55**	0.25	0.20	**2.61**	**2.59**	**0.67**	**0.75**	0.05	0.50
246-F3_C10_2	AC	0.17	0.11	**0.76**	**0.85**	**2.06**	**1.88**	0.19	0.19	0.14	0.27
CNE55	AE	0.42	0.05	**1.81**	**1.74**	**0.69**	0.27	0.45	0.11	0.00	0.17

Heterologous Strain	Clade	10397 Day 0	10397 Week 26 (182d)	10292 Day 0	10292 Week 27 (187d)	10802 Day 0	10802 Week 27 (187d)
YU2.DG	B	**0.90**	**1.04**	**0.60**	**0.65**	0.00	0.00
BaL.26	B	**3.15**	**3.16**	**2.68**	**2.55**	0.11	0.00
Q769.d22	A1	0.16	**0.74**	0.20	0.00	0.18	0.11
Q259.d2.17	A1	0.00	0.00	0.19	0.19	0.02	0.02
Q842.d12	A1	0.41	**0.60**	**0.63**	**0.66**	0.32	0.36
ZM135M.PL10a	C	0.02	0.00	0.00	0.00	0.01	0.08
25710-2.43	C	**0.96**	**0.70**	0.32	0.31	0.03	0.18
CNE8	AE	0.21	0.25	**0.52**	0.46	0.06	0.08
TRO.11	B	0.39	**0.60**	**0.71**	0.43	0.00	0.07
X1632_S2_B10	G	0.36	**0.65**	**0.74**	0.47	0.00	0.02
Ce1176_A3	C	0.14	0.19	0.15	0.16	**1.82**	**1.75**
246-F3_C10_2	AC	0.02	0.01	0.05	0.18	0.00	0.02
CNE55	AE	0.09	0.14	0.09	0.02	0.33	0.21

AUC
> 2
1-2
0.5 - 1
0 - 0.5

Table S4B.
Heterologous TZM.bl neutralization data of purified patient IgG (AUC), continued

Heterologous Strain	Clade	10099 Day 0	10099 Week 27 (187d)	10930 Day 0	10930 Week 27 (188d)	10417 Day 0	10417 Week 8 (56d)	10690 Day 0	10690 Week 16 (112d)	10257 Day 0	10257 Week 28 (196d)
YU2.DG	B	0.07	0.09	**1.24**	**1.08**	0.48	**0.51**	**1.31**	**1.37**	**0.75**	**0.83**
BaL.26	B	**1.81**	**1.95**	**2.77**	**2.72**	**3.24**	**3.31**	**2.38**	**2.16**	**2.44**	**2.40**
Q769.d22	A1	0.00	0.07	**1.27**	**1.06**	0.21	0.08	0.20	**0.52**	0.26	0.18
Q259.d2.17	A1	0.04	0.06	**0.86**	**0.60**	0.19	0.13	0.03	0.09	**0.50**	**0.87**
Q842.d12	A1	0.26	0.39	**1.85**	**1.61**	**0.59**	**1.03**	0.43	**0.63**	**1.26**	**1.69**
ZM135M.PL10a	C	0.06	0.06	0.08	0.01	**0.76**	**1.26**	0.19	0.15	**0.69**	**1.24**
25710-2.43	C	0.38	**0.64**	**0.65**	**0.54**	**1.01**	**1.41**	**0.73**	**0.77**	**0.97**	**1.48**
CNE8	AE	**0.56**	0.37	**2.33**	**2.18**	**1.88**	**2.21**	**0.54**	**0.54**	**0.99**	**1.18**
TRO.11	B	**0.81**	**0.85**	**1.53**	**1.19**	**1.48**	**1.64**	**1.06**	**1.02**	**1.69**	**1.77**
X1632_S2_B10	G	0.09	0.00	**1.68**	**1.29**	0.46	0.30	**0.81**	**1.18**	**0.61**	**0.90**
Ce1176_A3	C	**0.67**	0.41	**0.82**	**0.73**	**0.68**	**0.69**	**0.60**	**0.64**	0.28	0.31
246-F3_C10_2	AC	0.11	0.01	**1.82**	**1.75**	0.28	0.31	0.07	0.08	0.13	0.21
CNE55	AE	0.03	0.09	**1.57**	**1.54**	**0.64**	0.43	0.18	0.14	0.41	0.08

Heterologous Strain	Clade	10587 Day 0	10587 Week 17 (117d)	10169 Day 0	10169 Week 88 (617d)	10160 Day 0	10160 Week 15 (106d)	10811 Day 0	10811 Week 31 (215d)	10239 Day 0	10239 Week 35 (245d)
YU2.DG	B	0.40	0.29	**2.34**	**1.98**	**0.64**	**0.51**	0.43	0.48	0.21	0.20
BaL.26	B	**1.95**	**1.83**	**3.46**	**3.36**	**2.30**	**2.33**	**1.54**	**1.53**	**1.66**	**1.53**
Q769.d22	A1	**1.38**	**0.79**	**2.36**	**2.04**	0.44	0.28	0.21	**0.62**	0.12	0.49
Q259.d2.17	A1	0.18	0.21	**1.51**	**1.30**	0.16	0.03	0.04	0.10	0.12	0.01
Q842.d12	A1	**0.75**	**0.87**	**2.55**	**2.16**	0.26	0.20	0.39	**1.10**	0.23	0.22
ZM135M.PL10a	C	0.15	0.05	**1.70**	**0.98**	0.40	0.24	0.06	0.19	0.32	0.16
25710-2.43	C	0.49	0.42	**1.48**	**2.07**	**0.82**	**0.63**	**0.69**	**1.40**	**0.70**	**0.54**
CNE8	AE	0.28	0.35	**1.96**	**1.62**	0.41	0.32	0.07	0.25	0.18	0.12
TRO.11	B	**1.66**	**1.38**	**2.85**	**2.58**	**1.70**	**1.57**	**0.93**	**1.55**	0.29	0.26
X1632_S2_B10	G	**0.52**	0.49	**1.60**	**1.96**	0.40	**0.71**	0.29	0.16	0.35	0.19
Ce1176_A3	C	0.27	0.44	**1.47**	**1.14**	**0.83**	**0.69**	**0.66**	**1.31**	0.29	0.19
246-F3_C10_2	AC	0.04	0.07	**1.22**	**0.62**	0.08	0.07	0.16	**0.75**	0.21	0.10
CNE55	AE	**0.63**	**0.57**	**1.61**	**1.46**	0.40	**0.59**	**0.79**	**1.07**	0.41	0.29

Heterologous Strain	Clade	10814 Day 0	10814 Week 26 (181d)	10100 Day 0	10100 Week 11 (76d)	10779 Day 0	10779 Week 13 (89d)	10785 Day 0	10785 Week 31 (218d)	10489 Day 0	10489 Week 24 (169d)
YU2.DG	B	0.09	0.25	0.00	0.00	0.02	0.00	0.25	0.15	**0.70**	**0.63**
BaL.26	B	**1.21**	**0.99**	**1.36**	**1.30**	**2.81**	**2.54**	**2.19**	**2.05**	**2.11**	**2.31**
Q769.d22	A1	0.30	0.10	0.00	0.03	0.00	0.07	0.17	0.07	0.00	0.09
Q259.d2.17	A1	0.16	0.10	0.00	0.07	0.00	0.00	0.18	0.10	0.00	0.05
Q842.d12	A1	0.09	0.13	0.00	0.21	0.01	0.04	0.38	0.40	0.12	0.15
ZM135M.PL10a	C	0.20	0.34	0.00	0.00	0.25	0.25	0.29	0.25	0.11	0.10
25710-2.43	C	0.18	0.23	0.08	0.18	0.44	0.38	**1.14**	**1.14**	0.47	**0.60**
CNE8	AE	**0.79**	**0.81**	0.02	0.16	**0.70**	0.46	0.18	0.18	0.00	0.04
TRO.11	B	**1.11**	**1.05**	0.00	0.02	0.30	0.18	0.30	0.21	**1.68**	**1.59**
X1632_S2_B10	G	0.15	0.36	0.00	0.00	0.09	0.06	0.31	0.23	0.00	0.05
Ce1176_A3	C	0.29	0.35	0.20	0.01	0.08	0.19	0.36	0.38	0.21	0.29
246-F3_C10_2	AC	0.15	0.21	0.38	0.08	0.12	0.11	0.31	0.31	0.08	0.14
CNE55	AE	0.19	0.14	0.02	**0.87**	0.00	0.19	0.22	0.12	0.00	0.00

Heterologous Strain	Clade	10082 Day 0	10082 Week 30 (209d)	10914 Day 0	10914 Week 32 (224d)	10689 Day 0	10689 Week 27 (188d)
YU2.DG	B	0.08	0.00	**0.88**	0.28	0.10	0.08
BaL.26	B	**2.46**	**2.37**	**2.31**	**1.45**	**2.33**	**1.97**
Q769.d22	A1	0.13	0.01	0.08	0.20	**0.51**	0.22
Q259.d2.17	A1	0.06	0.04	0.02	0.01	0.26	0.25
Q842.d12	A1	0.06	0.00	0.13	0.04	0.44	0.35
ZM135M.PL10a	C	0.12	0.15	**0.77**	0.46	0.30	0.40
25710-2.43	C	0.11	0.07	**0.92**	**0.52**	0.44	0.45
CNE8	AE	0.00	0.00	**0.62**	0.25	0.01	0.00
TRO.11	B	0.45	0.20	**0.53**	0.20	0.16	0.24
X1632_S2_B10	G	0.13	0.13	0.08	0.00	0.03	0.00
Ce1176_A3	C	0.05	0.02	**0.60**	0.27	0.30	0.30
246-F3_C10_2	AC	0.10	0.11	0.18	0.10	0.24	0.31
CNE55	AE	0.00	0.00	0.00	0.00	0.20	0.11

AUC
> 2
1-2
0.5 - 1
0 - 0.5

Table S4B.
Heterologous TZM.bl neutralization data of purified patient IgG (AUC), continued
3BNC117-treated viremic patients

Heterologous Strain	Clade	2A1		2A3		2A4		2B1		2B3	
		Day -7	Week 24	Day 0	Week 24	Day -7	Week 24	Day -7	Week 24	Day -7	Week 24
YU2.DG	B	**2.51**	**2.60**	0.21	**0.61**	0.09	0.37	0.03	0.00	0.00	0.02
BaL.26	B	**3.72**	**3.70**	**2.35**	**2.55**	**1.41**	**1.64**	**1.03**	**0.94**	0.41	**0.52**
Q769.d22	A1	**1.72**	**1.64**	0.19	**2.40**	0.00	0.06	0.07	0.00	0.00	0.01
Q259.d2.17	A1	**0.91**	**1.76**	**1.02**	**1.61**	0.01	0.20	0.05	**0.51**	0.00	0.20
Q842.d12	A1	**2.53**	**2.67**	0.36	**0.56**	0.04	0.19	0.01	0.00	0.00	0.04
ZM135M.PL10a	C	0.25	**0.78**	0.12	0.32	0.01	0.12	0.09	0.08	0.00	0.22
25710-2.43	C	0.32	**0.73**	**0.96**	**1.33**	0.48	**0.58**	0.30	0.24	0.01	0.18
CNE8	AE	0.00	0.13	0.03	0.02	0.00	0.01	0.01	0.00	0.00	0.02
TRO.11	B	**1.04**	**1.88**	**0.67**	**1.10**	0.27	**0.70**	0.01	0.24	0.00	0.49
X1632_S2_B10	G	**1.66**	**1.91**	0.22	0.29	0.06	0.10	0.09	0.00	0.00	0.04
Ce1176_A3	C	0.00	0.28	0.21	0.44	0.00	0.16	0.02	0.15	0.01	0.14
246-F3_C10_2	AC	*N/A*	*N/A*	**0.53**	**0.60**	*N/A*	*N/A*	*N/A*	*N/A*	*N/A*	*N/A*
CNE55	AE	0.34	**0.81**	0.12	0.13	0.00	0.00	0.03	0.00	0.02	0.02

Heterologous Strain	Clade	2C4		2C5		2D1		2C1		2D3	
		Day -7	Week 24	Day -7	Week 24	Day 0	Week 24	Day -7	Week 24	Day -7	Week24
YU2.DG	B	**1.10**	**1.64**	0.04	0.11	0.16	0.06	0.14	0.15	0.00	0.14
BaL.26	B	**2.10**	**2.81**	**2.16**	**2.75**	**1.11**	**1.45**	**1.18**	**1.71**	0.00	0.26
Q769.d22	A1	0.03	0.43	0.08	0.38	0.04	0.26	0.24	0.28	0.01	**0.61**
Q259.d2.17	A1	*N/A*	*N/A*	*N/A*	*N/A*	0.20	0.20	0.07	0.42	0.01	0.25
Q842.d12	A1	**1.42**	**1.36**	0.02	0.12	0.09	0.23	0.19	**0.59**	0.00	0.46
ZM135M.PL10a	C	0.11	**0.55**	0.13	**0.86**	0.16	0.24	0.09	0.23	0.09	0.31
25710-2.43	C	**0.62**	**1.88**	**0.55**	**0.98**	0.38	0.29	0.47	**1.15**	0.01	0.00
CNE8	AE	0.47	**1.48**	0.06	**0.79**	0.00	0.00	0.03	0.16	0.00	0.02
TRO.11	B	**1.61**	**2.86**	0.38	**0.83**	0.34	0.15	0.16	0.42	0.02	0.12
X1632_S2_B10	G	0.13	**0.80**	0.08	0.42	0.18	0.05	0.13	0.15	0.01	0.03
Ce1176_A3	C	0.24	**1.53**	0.00	0.04	0.12	0.00	0.04	0.07	0.08	0.00
246-F3_C10_2	AC	*N/A*	*N/A*	*N/A*	*N/A*	0.22	0.02	*N/A*	*N/A*	0.18	0.00
CNE55	AE	0.04	0.07	0.02	0.00	0.00	0.01	0.04	0.00	0.02	0.08

Heterologous Strain	Clade	2E1		2E2		2E3		2E4		2E5	
		Day 0	Week 24	Day 0	Week 24	Day 0	Week 24	Day 0	Week 24	Day 0	Week 24
YU2.DG	B	0.00	0.28	0.08	0.30	0.00	0.13	0.28	**0.52**	0.00	**0.53**
BaL.26	B	**1.40**	**2.12**	**2.24**	**2.71**	**1.27**	**2.33**	**1.26**	**1.74**	**0.63**	**1.77**
Q769.d22	A1	0.48	**1.05**	0.00	0.50	0.00	**0.80**	0.47	0.40	0.17	**0.73**
Q259.d2.17	A1	0.03	0.24	0.30	0.14	0.30	0.18	0.34	**0.62**	0.13	**0.73**
Q842.d12	A1	0.02	0.19	0.12	0.19	0.16	0.24	0.36	**0.59**	0.25	**0.56**
ZM135M.PL10a	C	0.00	0.14	0.24	0.13	0.15	0.37	**0.53**	0.35	0.12	0.21
25710-2.43	C	**0.60**	**0.65**	0.47	0.46	0.42	**0.61**	**1.02**	**0.99**	0.07	0.22
CNE8	AE	0.05	0.07	0.03	0.15	0.04	0.02	**0.93**	**1.32**	0.05	0.10
TRO.11	B	**0.65**	**1.14**	0.40	0.18	0.34	0.38	**0.99**	**0.80**	0.14	0.30
X1632_S2_B10	G	0.16	0.26	0.22	0.41	0.01	0.32	0.21	0.30	0.04	**0.51**
Ce1176_A3	C	0.21	0.02	0.12	0.00	0.05	0.00	0.34	0.13	0.12	0.15
246-F3_C10_2	AC	0.18	**0.51**	0.39	0.14	0.17	0.14	**0.83**	**0.57**	0.19	**1.13**
CNE55	AE	0.00	0.00	*N/A*	*N/A*	0.00	0.00	0.00	0.00	0.00	0.03

AUC
> 2
1-2
0.5 - 1
0 - 0.5

Table S4B.
Heterologous TZM.bl neutralization data of purified patient IgG (AUC), continued
3BNC117-treated patients on-ART

Heterologous Strain	Clade	5A1 Day 0	5A1 Week 24	5A2 Day 0	5A2 Week 24	5A3 Day 0	5A3 Week 24	5A4 Day 0	5A4 Week 24	5A5 Day 0	5A5 Week 24
YU2.DG	B	0.04	0.02	0.03	0.01	0.07	0.18	0.04	0.03	0.06	0.05
BaL.26	B	0.05	0.02	**0.91**	**0.87**	**1.30**	**2.31**	0.26	0.44	0.12	0.11
Q769.d22	A1	0.01	0.46	0.01	0.20	0.01	0.07	0.03	0.18	0.21	0.20
Q259.d2.17	A1	0.20	0.21	0.09	0.27	0.33	0.41	0.23	0.20	0.09	0.20
Q842.d12	A1	0.18	0.29	0.25	0.29	0.20	**0.52**	0.36	0.38	0.18	0.34
ZM135M.PL10a	C	0.00	0.09	0.01	0.21	0.07	0.07	0.17	0.05	0.04	0.04
25710-2.43	C	0.01	0.08	0.05	0.23	0.12	0.23	0.18	0.17	0.42	0.46
CNE8	AE	0.00	0.00	0.00	0.03	0.01	0.13	0.02	0.00	0.09	0.08
TRO.11	B	0.11	0.09	0.17	0.05	0.36	0.49	0.12	0.11	0.24	0.27
X1632_S2_B10	G	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.05	0.14	0.09
Ce1176_A3	C	0.00	0.00	0.03	0.00	0.00	0.12	0.00	0.02	0.03	0.02
246-F3_C10_2	AC	0.03	0.01	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.00
CNE55	AE	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Heterologous Strain	Clade	5B1 Day 0	5B1 Week 24	5B2 Day 0	5B2 Week 24	5B3 Day 0	5B3 Week 24	5B4 Day 0	5B4 Week 24	5B5 Day 0	5B5 Week 24
YU2.DG	B	0.00	0.02	0.03	0.11	0.00	0.02	0.07	0.05	0.28	0.19
BaL.26	B	**1.18**	**1.22**	**1.37**	**1.10**	0.15	0.21	**1.77**	**1.85**	**1.32**	**1.43**
Q769.d22	A1	0.00	0.00	**0.54**	**0.57**	0.27	0.14	0.30	0.41	**0.73**	**0.99**
Q259.d2.17	A1	0.00	0.10	0.18	0.11	0.00	0.05	0.01	0.04	0.29	0.23
Q842.d12	A1	0.10	0.08	0.18	0.41	0.08	0.20	0.19	0.12	**0.56**	**0.59**
ZM135M.PL10a	C	0.00	0.02	0.18	0.13	0.03	0.14	0.18	0.25	0.30	**0.52**
25710-2.43	C	0.14	0.20	0.29	0.21	0.06	0.08	0.18	0.20	0.48	0.44
CNE8	AE	0.02	0.00	0.05	0.04	0.00	**0.80**	0.04	**0.84**	0.26	**1.08**
TRO.11	B	0.00	0.01	0.13	0.12	0.00	0.37	0.06	0.21	0.26	**0.87**
X1632_S2_B10	G	0.00	0.00	0.10	0.19	0.00	0.36	0.04	0.41	0.07	**0.80**
Ce1176_A3	C	0.01	0.04	0.08	0.10	0.06	0.13	0.12	0.09	0.10	**0.53**
246-F3_C10_2	AC	0.03	0.11	0.12	0.15	0.07	0.24	0.16	0.25	0.14	**0.80**
CNE55	AE	0.00	0.00	0.07	0.25	0.16	0.26	0.14	0.26	0.14	**1.08**

Heterologous Strain	Clade	2B2 Day -7	2B2 Week 24	2C2 Day -7	2C2 Week 24
YU2.DG	B	0.00	0.03	0.00	0.02
BaL.26	B	**0.68**	**0.71**	**1.03**	**1.40**
Q769.d22	A1	0.20	0.00	0.01	0.07
Q259.d2.17	A1	0.00	0.09	0.00	0.29
Q842.d12	A1	0.00	0.14	0.04	0.30
ZM135M.PL10a	C	0.11	0.14	0.16	0.29
25710-2.43	C	0.39	0.49	0.28	**0.65**
CNE8	AE	0.00	0.03	0.00	0.12
TRO.11	B	0.04	0.30	0.11	**0.74**
X1632_S2_B10	G	0.14	0.08	0.07	0.23
Ce1176_A3	C	0.02	0.07	0.12	0.22
246-F3_C10_2	AC	*N/A*	*N/A*	*N/A*	*N/A*
CNE55	AE	0.23	0.00	0.27	0.02

AUC
> 2
1-2
0.5 - 1
0 - 0.5

Table S5A.
Summary measures table breadth and potency Day 0 and Wk24
Untreated viremic control individuals

		Breadth				Overall neutralizing activity (Potency and breadth)	
Subject ID	**Status before therapy**	**Number of viruses neutralized with AUC > 0.5 pre-therapy**	**Percent of viruses neutralized with AUC > 0.5 pre-therapy**	**Number of viruses neutralized with AUC > 0.5 post-therapy**	**Percent of viruses neutralized with AUC > 0.5 post-therapy**	**Mean AUC Day 0**	**Mean AUC Wk 24**
Untreated viremic control individuals							
10518	Control	2	15%	3	23%	0.305	0.413
10362	Control	2	15%	2	15%	0.393	0.352
10112	Control	11	92%	12	100%	1.809	1.692
10962	Control	13	100%	13	100%	1.492	1.536
10223	Control	13	100%	13	100%	1.595	1.497
10482	Control	4	31%	4	31%	0.407	0.423
10210	Control	5	38%	5	38%	0.594	0.537
10596	Control	9	69%	7	54%	1.096	0.962
10138	Control	11	85%	11	85%	1.634	1.566
10108	Control	13	100%	13	100%	2.739	2.701
10275	Control	1	8%	3	23%	0.409	0.422
10959	Control	8	62%	8	62%	1.186	1.193
10367	Control	11	85%	9	69%	1.645	1.514
10469	Control	8	62%	8	62%	0.724	0.676
10410	Control	1	8%	2	15%	0.267	0.396
10397	Control	3	23%	7	54%	0.525	0.623
10292	Control	6	46%	3	23%	0.530	0.468
10802	Control	1	8%	1	8%	0.222	0.225
10099	Control	4	31%	3	23%	0.376	0.384
10930	Control	12	92%	12	92%	1.420	1.254
10417	Control	8	62%	8	62%	0.915	1.023
10690	Control	7	54%	9	69%	0.656	0.714
10257	Control	9	69%	9	69%	0.845	1.009
10587	Control	6	46%	5	38%	0.669	0.598
10169	Control	13	100%	13	100%	2.009	1.789
10160	Control	5	38%	7	54%	0.682	0.627
10811	Control	5	38%	8	62%	0.481	0.807
10239	Control	2	15%	2	15%	0.391	0.330
10814	Control	3	23%	3	23%	0.378	0.390
10100	Control	1	8%	2	15%	0.159	0.225
10779	Control	2	15%	1	8%	0.371	0.343
10785	Control	2	15%	2	15%	0.482	0.429
10489	Control	3	23%	4	31%	0.422	0.465
10082	Control	1	8%	1	8%	0.288	0.238
10914	Control	7	54%	2	15%	0.548	0.291
10689	Control	2	15%	1	8%	0.410	0.359
Average :		5.1	39.1%	5.1	39.1%	0.7	0.6

Table S5B.
Summary measures table breadth and potency Day 0 and Wk24
3BNC117-treated individuals

		Breadth				Overall neutralizing activity (Potency and breadth)	
Subject ID	**Status before therapy**	**Number of viruses neutralized with AUC > 0.5 pre-therapy**	**Percent of viruses neutralized with AUC > 0.5 pre-therapy**	**Number of viruses neutralized with AUC > 0.5 post-therapy**	**Percent of viruses neutralized with AUC > 0.5 post-therapy**	**Mean AUC Day 0**	**Mean AUC Wk 24**
Viremic individuals							
2A1	Viremic	7	58%	10	83%	1.250	1.575
2A3	Viremic	5	38%	8	62%	0.537	0.921
2A4	Viremic	1	8%	3	25%	0.196	0.345
2B1	Viremic	1	8%	2	17%	0.144	0.180
2B3	Viremic	0	0%	1	8%	0.038	0.159
2C4	Viremic	5	45%	9	82%	0.717	1.403
2C5	Viremic	2	18%	5	45%	0.321	0.662
2D1	Viremic	1	8%	1	8%	0.230	0.227
2C1	Viremic	1	8%	3	25%	0.232	0.444
2D3	Viremic	0	0%	1	8%	0.033	0.176
2E1	Viremic	3	23%	5	38%	0.292	0.513
2E2	Viremic	1	8%	1	8%	0.384	0.442
2E3	Viremic	1	8%	3	23%	0.224	0.425
2E4	Viremic	6	46%	8	62%	0.581	0.641
2E5	Viremic	1	8%	7	54%	0.147	0.537
Average :		2.3	19.1%	4.5	36.5%	0.4	0.6
Individuals on-ART							
5A1	on-ART	0	0%	0	0%	0.0482	0.0976
5A2	on-ART	1	8%	1	8%	0.1204	0.1665
5A3	on-ART	1	8%	2	15%	0.1897	0.3528
5A4	on-ART	0	0%	0	0%	0.1090	0.1259
5A5	on-ART	0	0%	0	0%	0.1255	0.1437
5B1	on-ART	1	8%	1	8%	0.1137	0.1382
5B2	on-ART	2	15%	2	15%	0.2535	0.2679
5B3	on-ART	0	0%	1	8%	0.0685	0.2294
5B4	on-ART	1	8%	2	15%	0.2510	0.3820
5B5	on-ART	3	23%	10	77%	0.3799	0.7352
2B2	on-ART	1	8%	1	8%	0.1501	0.1726
2C2	on-ART	1	8%	3	25%	0.1753	0.3616
Average :		1.0	8.1%	2.1	16.6%	0.2	0.3

Table S6.
TZM.bl neutralization data over time in subject 2A3 (IC50)

Heterologous strain	Clade	Day 0	Week 12	Week 16	Week 20	Week 24
YU2.DG	B	>500	**483.2**	**403.7**	**390.1**	**363.4**
BaL.26	B	**28.4**	**24.2**	**25.5**	**24.3**	**18.9**
Q769.d22	A1	>500	**452.0**	**266.2**	**82.8**	**19.4**
Q259.d2.17	A1	**92.5**	**61.4**	**71.9**	**93.0**	**84.7**
Q842.d12	A1	**475.0**	**499.7**	**436.0**	**426.8**	**417.8**
ZM135M.PL10a	C	>500	>500	>500	>500	>500
25710-2.43	C	**110.8**	**109.7**	**159.8**	**123.1**	**136.0**
CNE8	AE	>500	>500	>500	>500	>500
TRO.11	B	**218.6**	**435.4**	**401.5**	**257.5**	**203.0**
X1632_S2_B10	G	>500	>500	>500	>500	>500
Ce1176_A3	C	**482.2**	>500	**493.4**	**432.9**	**446.7**
246-F3_C10_2	AC	**445.4**	**430.4**	**420.3**	**299.9**	**283.7**
CNE55	AE	>500	>500	>500	>500	>500

IgG IC_{50} titers (µg/ml)

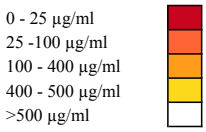

Table S7.
Analysis of potential confounding variables

	Variable (p-value of likelihood ratio test if alternative model superior to null-model)							
AUC change observed in viral strain	**Age**	**Time since diagnosis**	**Sampling interval**	**abs. $CD4^+$ T cell count ($cells/mm^3$) Day 0**	**abs. $CD4^+$ T cell count ($cells/mm^3$) Week 24**	**HIV-RNA level (copies/ml) Day 0**	**HIV-RNA level (copies/ml) Week 24**	**Starting AUC (AUC Day 0)**
246.F3_C10_2	1	1	1	1	1	1	1	1
CNE55	1	1	0.18	1	1	1	1	0.18
Ce1176_A3	1	1	1	1	1	1	1	1
TRO.11	1	1	0.41	1	1	1	0.23	1
Q259.d2.17	1	1	0.10	1	1	1	1	1
25710-2.43	1	1	1	1	1	1	1	0.66
Q769.d22	1	1	0.64	1	1	1	1	0.50
BaL.26	1	0.50	0.02	1	0.09	1	1	0.47
YU.2	1	1	0.52	1	1	1	0.69	1
X1632_S2_B10	1	1	0.05	1	1	1	0.92	0.17
ZM135M.PL10a	1	1	0.37	1	1	1	1	1
Q842.d12	1	1	1	1	0.56	1	1	0.0035
CNE8	0.46	1	0.58	1	1	1	1	1

Bonferroni-corrected significance threshold: 0.0005 with significance level $\alpha = 0.05$

variable is not predictive of AUC change

Table S8.
Rank correlation and p-values for Spearman rank correlation of patient and 3BNC117 neutralization

Subject ID	rank correlation (AUC-based)	p-value (AUC-based)	rank correlation (IC_{50}-based)	p-value (IC_{50}-based)
2A1	0.46	0.1689	-0.43	0.1369
2A3	-0.33	0.2470	0.35	0.2664
2A4	-0.52	0.1926	0.41	0.0818
2B1	0.02	0.9224	-0.03	0.9611
2B3	0.14	0.5135	-0.21	0.6641
2C4	0.39	0.2250	-0.40	0.2334
2C5	-0.12	0.8815	0.05	0.7287
2D1	-0.65	0.0103	0.70	0.0163
2C1	-0.30	0.3425	0.30	0.3355
2D3*	-0.84	0.0001	0.87	0.0003
2E1	-0.62	0.0160	0.66	0.0225
2E2	-0.43	0.1926	0.41	0.1659
2E3	-0.24	0.5292	0.19	0.4364
2E4	-0.48	0.0850	0.50	0.1002
2E5	-0.38	0.1013	0.48	0.1972
2B2	-0.14	0.8690	0.06	0.6641
2C2	-0.09	0.8517	0.06	0.7700
5A1	0.00	0.8922	0.04	1.0000
5A2	0.12	0.9786	-0.01	0.7029
5A3	-0.60	0.1013	0.48	0.0293
5A4	-0.19	0.4930	0.21	0.5339
5A5	-0.21	0.4561	0.23	0.4988
5B1	0.23	0.6138	-0.15	0.4505
5B2	0.01	0.8632	-0.05	0.9644
5B3	0.24	0.3103	-0.31	0.4330
5B4	0.26	0.5785	-0.17	0.3936
5B5	0.43	0.1955	-0.38	0.1377

p-value threshold (Bonferroni-corrected): 0.0019

*Significant rank correlation only detected in 2D3 (indicated in green).

Table S9.
Number of gp160 nucleotide sequences included in phylogenetic analysis

Subject	Day 0	Week 4 (6)	Week 12	Week 24	Total per patient
2A1	27	26	24	40	117
2A3	23	32	29	27	111
2C4	33	19	30	19	101
2C5	48	20	22	32	122
2E1	30	31	27	37	125
2E2	20	27	25	27	99
2E3	25	17	24	21	87
2E4	41	25	26	29	121
2E5	47	3 (22*)	23	22	117
Total per TP	294	222	230	254	1000

(*) due to low viral load week 6 plasma was sequenced

Table S10.
Envelope amino acid residues under significant selection in each individual

Subject ID	Sites Under Selection (≥80% different from Day 0 Consensus)
2A1	12,134-6, 138-46, 148-9, 149lmopstuv, 150-3, 155, 161, 164, 166, 168-71, 177, 178, 182, 185-188, 189bdef, 195, 209, 240, 270, 272, 279*, 283, 287, 291, 293, 306, 316-7, 318, 321a, 326, 333, 335, 336-7, 343, 344, 346-7, 360, 362, 364, 365, 373, 386, 395, 398, 401-5, 408, 411-3, 417, 442, 460, 461, 471, 698
2A3	137-8, 140, 141af, 142, 187e, 336, 410
2C4	59, 188ckl, 283, 308, 339, 346-7, 354, 356, 362, 386, 389, 392-6, 400-5, 410, 415, 459abhijkl, 640, 674, 689, 742
2C5	140, 275, 279, 290, 340, 344, 347, 350, 353, 355, 364a, 396, 397, 400-3, 405-7, 409, 461, 461abce, 464, 465, 500
2E1	141, 147-9, 150b, 160, 398, 401-4, 410, 460, 463, 500, 624
2E2	153, 295, 297, 344, 397-8, 411, 413, 444, 461, 636
2E3	32, 145, 440, 464, 683
2E4	187dehi, 337, 340, 343
2E5	80, 282, 400

*3BNC117 contact sites confirmed by crystal structures (*25,26*) are in red

Table S11.
TZM.bl neutralization data of CMV-env pseudotyped viruses (IC_{50})

Subject ID	Virus ID (in order of appearance in tree top to bottom)	3BNC117 IC_{50} (µg/ml)	Day 0 IgG IC_{50} (µg/ml)	Week 24 IgG IC_{50} (µg/ml)
2A1	2A1-D0-0408TIT-E5_S57	0.119	101.1	33.4
	2A1_D0_0409_G3_S89	0.209	333.6	66.6
	2A1-D0-0409-B1_S73	0.116	161.5	70.1
	2A1-W4-0408TIT-G11_S19	0.157	233.4	109.2
	2A1-D0-0409-E7_S85	0.141	96.9	94.5
	2A1-W24-0409-H4_S33	0.306	185.1	199.5
	2A1-W24-0409-E1_S22	0.641	171.3	157.6
	2A1-W12-TIT0402-D1_S36	0.691	154.3	160.3
	2A1-W24-0409-G11_S30	0.585	175.6	187.1
	2A1-D0-0409-C2_S77	0.692	149.4	135.1
	2A1-W4-0408TIT-H2_S16	0.595	164.2	153.9
	2A1-D0-0409-G9_S90	0.651	165.8	154.5
	2A1-W4-0408TIT-E12-S4	0.184	198.4	96.3
	2A1-W4-0408TIT-G9_S12	0.181	266.1	143.2
	2A1-W4-0408TIT-G10_S13	0.128	164.9	85.4
	2A1-D0-0409-B4-S74	0.317	423.9	186.6
	2A1-W24-0409-H11_S34	0.240	176.1	113.6
	2A1-W4-0408TIT-F8_S6	0.159	239.1	127.1
	2A1-D0-0409-H9_S93	0.008	123.4	139.4
	2A1-D0-0409-E5_S83	0.017	187.2	180.6
2E1	2E1-D0-0409-E4_S58	0.038	107.7	77.3
	2E1-W4_G11_S39	0.185	257.7	23.8
	2E1-W4-TIT0408-D3_S63	0.048	338.1	29.1
	2E1-D0-0409-H8_S69	0.124	211.0	73.6
	2E1-W4-TIT0408-D7_S64	0.106	384.6	38.0
	2E1-W12-0409-H3_S20	0.025	>500.0	233.5
	2E1-W12-0409-G3_S16	0.063	>500.0	>500.0
	2E1-W24-0526PlE-A9_S72	0.052	333.9	154.8
	2E1-W24-0526PlE-B3_S74	0.080	>500.0	452.1
	2E1-D0-0421-G4_S4	0.091	421.4	97.6
	2E1-W4-TIT0408-E7_S69	0.078	360.5	33.5
	2E1-W12-0524Pl2-F6_S49	0.087	>500.0	94.6
	2E1-W24-0526PlE-G6_S85	0.064	266.7	189.6
	2E1-W24-0526PlE-F1e_S80	0.040	370.5	197.9
2C5	2C5-W24-0423-H6_S78	>20	22.5	30.2
	2C5-D0-0422-H4-S56	0.006	36.4	35.9
	2C5-D0-0422-F4-S44	0.011	20.3	34.5
	2C5-W24-0423-F2-S73	0.022	145.7	500.0
	2C5-W4-0423-A6-S33	3.131	18.1	20.6
	2C5-W4-0423-D11_S38	14.079	49.9	12.2
	2C5-W12-TIT0418-D2_S6	1.142	2.5	2.8
	2C5-W4-0422-G1_S91	>20	85.1	38.1
2A3	2A3-W24-TIT0406-B6_S68	0.195	>500.0	407.2
	2A3_D0_0404_C9_S75	0.055	543.9	210.4
	2A3-D0-0421-A3_S44	0.171	>500.0	>500.0
	2A3-W4-0421-E11_S55	1.024	255.2	218.5
	2A3-W24-TIT0406-B7_S69	0.022	411.3	419.5
	2A3-W24-TIT0406-A6e_S65	0.071	292.9	327.8
	2A3-W12-0421-A7_S84	0.051	255.2	182.0
	2A3-D0-0421-D3_S50	0.037	305.6	212.7
	2A3-W24-TIT0406-C11_S74	0.049	224.0	223.0
	2A3-W12-0421-C12_S94	0.055	293.6	263.7
	2A3-W12-0406-F2_S50	0.049	276.5	168.6
	2A3-W4-0406-E12_S31	0.030	169.3	11.1
	2A3_D0_0404_C1_S74	0.074	447.4	155.9
	2A3-W4-0406-A3_S14	0.099	>500.0	219.3
2C4	2C4-W24-0406-A5_S65	>20	240.8	36.1
	2C4-W24-0406-H10_S88	>20	156.7	39.2
	2C4-W24-0406-D6_S74	>20	153.9	39.0
	2C4-D0-0404-C1_S30	>20	195.7	21.9
	2C4-D0-0406-H7_S24	>20	155.3	20.7
	2C4-D0-0406-F3_S19	>20	147.6	20.4
	2C4-D0-0406-E10_S18	>20	170.9	23.8

3BNC117 IC_{50} (µg/ml)	IgG IC_{50} (µg/ml)
0 - 0.1	0 - 50
0.1 - 0.5	50 -100
0.5 - 1.0	100 - 150
1.0 - 2.0	150 - 200
2.0 - 5.0	200 - 250
5.0 - 10.0	250 - 500
> 10.0	> 500

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